

WEST Search History

DATE: Thursday, February 15, 2007

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L10	CXCR4 NEAR (antibody or antibodies) AND (vascularization OR neovascularization OR vascularize)	271
<input type="checkbox"/>	L9	L8 AND (vascularization OR neovascularization OR vascularize)	11
<input type="checkbox"/>	L8	L6 AND (seven-transmembrane)	42
<input type="checkbox"/>	L7	L6 AND (leukocyte-derived)	0
<input type="checkbox"/>	L6	LESTR AND antibody AND cancer	147
<input type="checkbox"/>	L5	PF4A AND IL-8 AND antibody AND (vascularization OR neovascularization OR vascularize)	3
<input type="checkbox"/>	L3	L2 AND antibody	23
<input type="checkbox"/>	L2	PF4A AND IL-8 AND tumor	23
<input type="checkbox"/>	L1	PF4A AND IL-8 AND cancer	6

END OF SEARCH HISTORY

10	1830	100.0	352	2	US-09-517-605-4	Sequence 4, Appli
11	1830	100.0	352	2	US-09-647-501-2	Sequence 2, Appli
12	1824	99.7	352	2	US-09-826-509-485	Sequence 485, App
13	1789	97.8	352	1	US-08-450-393A-6	Sequence 6, Appli
14	1789	97.8	352	2	US-08-446-669-6	Sequence 6, Appli
15	1789	97.8	352	2	US-09-625-573-6	Sequence 6, Appli
16	1789	97.8	352	5	PCT-US95-00476-6	Sequence 6, Appli
17	1752	95.7	337	1	US-08-153-848-46	Sequence 46, Appl
18	1752	95.7	337	2	US-09-299-843A-46	Sequence 46, Appl
19	1752	95.7	337	2	US-09-088-337B-46	Sequence 46, Appl
20	1752	95.7	337	5	PCT-US93-11153-46	Sequence 46, Appl
21	614	33.6	116	2	US-09-513-999C-5992	Sequence 5992, Ap
22	600.5	32.8	360	2	US-08-875-573-20	Sequence 20, Appl
23	600.5	32.8	360	2	US-09-232-878-2	Sequence 2, Appli
24	600.5	32.8	360	2	US-09-045-583-55	Sequence 55, Appl
25	600.5	32.8	360	2	US-09-534-185-55	Sequence 55, Appl
26	600.5	32.8	360	2	US-08-939-107-34	Sequence 34, Appl
27	600.5	32.8	360	2	US-10-039-659A-16	Sequence 16, Appl
28	600.5	32.8	360	2	US-09-067-447B-34	Sequence 34, Appl
29	600.5	32.8	360	2	US-09-837-446-2	Sequence 2, Appli
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32	600.5	32.8	360	3	US-09-509-165A-34	Sequence 34, Appl
33	594	32.5	123	2	US-08-513-974B-330	Sequence 330, App
34	588.5	32.2	360	2	US-08-833-752-10	Sequence 10, Appl
35	588.5	32.2	360	2	US-09-938-719-10	Sequence 10, Appl
36	588.5	32.2	360	2	US-09-939-226B-10	Sequence 10, Appl
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43	576.5	31.5	368	3	US-09-633-541-2	Sequence 2, Appli
44	572.5	31.3	368	2	US-09-170-496D-174	Sequence 174, App
45	569	31.1	367	2	US-10-244-089-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-202-056-3

; Sequence 3, Application US/08202056

; Patent No. 5440021

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Hebert, Caroline

; APPLICANT: Kim, Kyung Jin

; APPLICANT: Lee, James

; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/202,056

; FILING DATE: 25-FEB-1994

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: 706P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-202-056-3

Query Match 100.0%; Score 1830; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8e-143;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
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RESULT 2

US-08-076-093A-4

; Sequence 4, Application US/08076093A
 ; Patent No. 5543503
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Lee, James
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Jin Kim, K.
 ; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/076,093A
 ; FILING DATE: 11-Jun-1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/810782
 ; FILING DATE: 19-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; FILING DATE: 29-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: 706P2


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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-076-093A-4
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Query Match      100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MEGISIIYSDNYTEEMSGDYDSMKPEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

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Db    121 YSSVLILAFISLDRLYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
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RESULT 3
US-08-701-265-4
; Sequence 4, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-701-265-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
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Db    121 YSSVLILAFISLD RYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGHKQRKALKT 240
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Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALT SVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 4
US-08-284-586-4
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; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-284-586-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYSDNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGVGNGLVI 60
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Db      1 MEGISIIYSDNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
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Qy    241 TVILILAFFACWLPYYIGISIDSFILEIISKQCEFENTVHKWISITEALAFFHCCLNPI 300
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Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
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RESULT 5
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-805-478-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Db      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240
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Db    181 DDYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
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RESULT 6

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US-08-802-627A-4
; Sequence 4, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-802-627A-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKPEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKPEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKV VYGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKV VYGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240
        |||
Db    181 DDRIYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 7

US-08-801-238-4

; Sequence 4, Application US/08801238

; Patent No. 5919896

; GENERAL INFORMATION:

; APPLICANT: Lee, James

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PF4A RECEPTOR

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/801,238

; FILING DATE: 19-Feb-1997

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-238-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity. 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYSDNYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYSDNYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYCDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DDRIYCDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 8

US-08-801-228-4

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; Sequence 4, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-4

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Query Match          100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60

Qy     61 LVMGYQKKLRSMIDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVMGYQKKLRSMIDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 9

US-09-104-296-4

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; Sequence 4, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-104-296-4

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Query Match          100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLT GIVGNGLVI 60
        |||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLT GIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||||||
Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240
        |||||||
Db    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        |||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 10

US-09-517-605-4

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; Sequence 4, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02

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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-4

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKV VYGVWIPALLLTIPDFIFANVSEA 180
        |||||||
Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKV VYGVWIPALLLTIPDFIFANVSEA 180

Qy    181 D DRYICDRFY PNDLWVVVFQFQHIMVGLILPGIVILSCYCI IISKLSHSGHQKRKALKT 240
        |||||||
Db    181 D DRYICDRFY PNDLWVVVFQFQHIMVGLILPGIVILSCYCI IISKLSHSGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALT SVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||||||
Db    301 LYAFLGAKFKTSAQHALT SVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
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RESULT 11

US-09-647-501-2
; Sequence 2, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
; APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT APPLICATION NUMBER: US/09/647,501
; CURRENT FILING DATE: 2000-09-24
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-647-501-2

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKV VYGVWIPALLLTIPDFIFANVSEA 180
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Db      121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
Qy      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
Db      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLNPI 300
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLNPI 300
Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 352
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 352

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RESULT 12

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US-09-826-509-485
; Sequence 485, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-485

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Query Match      99.7%; Score 1824; DB 2; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.2e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTSNDYTEEMSGSDYDSMKPECFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
Db      1 MEGISIIYTSNDYTEEMSGSDYDSMKPECFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
Qy      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
Db      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
Qy      121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
Db      121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
Qy      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
Db      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLNPI 300
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLNPI 300
Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 352
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 352

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RESULT 13

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US-08-450-393A-6
; Sequence 6, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel

```

; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

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9	1830	100.0	352	5	ABP52651	Abp52651	Human	CXC
10	1830	100.0	352	5	ABG32977	Abg32977	Human	CXC
11	1830	100.0	352	5	ABG33065	Abg33065	Human	CXC
12	1830	100.0	352	5	ABP65183	Abp65183	Hypoxia-r	
13	1830	100.0	352	5	AAG78471	Aag78471	CXCR4	pro
14	1830	100.0	352	6	ABP96794	Abp96794	Human	COP
15	1830	100.0	352	6	ABU03495	Abu03495	Angiogene	
16	1830	100.0	352	6	ABR58581	Abr58581	Human	can
17	1830	100.0	352	6	ABP97733	Abp97733	Amino	aci
18	1830	100.0	352	6	ABP81796	Abp81796	Human	CXC
19	1830	100.0	352	7	ADC98646	Adc98646	Human	CXC
20	1830	100.0	352	7	ADE63147	Ade63147	Human	Pro
21	1830	100.0	352	7	ADE63143	Ade63143	Human	Pro
22	1830	100.0	352	7	ADF90878	Adf90878	Human	hep
23	1830	100.0	352	7	ADO16837	Ado16837	CXCR4	ami
24	1830	100.0	352	7	ADN95821	Adn95821	Human	BEC
25	1830	100.0	352	8	ADH17079	Adh17079	Human	orp
26	1830	100.0	352	8	ADN04756	Adn04756	Antipsori	
27	1830	100.0	352	8	ADO29271	Ado29271	Human	GPC
28	1830	100.0	352	8	ADP12477	Adp12477	Protein	e
29	1830	100.0	352	8	ADP12926	Adp12926	Protein	e
30	1830	100.0	352	8	ADP13001	Adp13001	Protein	e
31	1830	100.0	352	8	ADO19692	Ado19692	Human	PRO
32	1830	100.0	352	8	ADO19832	Ado19832	Human	PRO
33	1830	100.0	352	8	ADO20013	Ado20013	Human	PRO
34	1830	100.0	352	8	ADP44055	Adp44055	Human	CXC
35	1830	100.0	352	8	ADQ14488	Adq14488	Human	che
36	1830	100.0	352	8	ADQ97944	Adq97944	Human	can
37	1830	100.0	352	8	ADR51540	Adr51540	Human	lip
38	1830	100.0	352	8	ADR87598	Adr87598	Human	CXC
39	1830	100.0	352	9	ADY19742	Ady19742	PRO	polyp
40	1830	100.0	352	9	ADY16664	Ady16664	PRO	polyp
41	1830	100.0	352	9	ADY17210	Ady17210	PRO	polyp
42	1830	100.0	352	9	ADY16155	Ady16155	PRO	polyp
43	1830	100.0	352	9	AED15419	Aed15419	Equine	Pr
44	1830	100.0	352	9	AED76716	Aed76716	CXCR4	rec
45	1830	100.0	352	10	AEE66168	Aee66168	Human	CXC

ALIGNMENTS

RESULT 1

AAR68812

ID AAR68812 standard; protein; 352 AA.

XX

AC AAR68812;

XX

DT 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX

DE Human monocyte PF4AR.

XX

KW Interleukin-8 receptor; IL-8 receptor; PF4AR;

KW platelet factor superfamily receptor; monocyte; chemotactic;

KW inflammation; inflammatory disease; arthritis; emphysema; cystic;

KW fibrosis; colitis; bronchitis; meningitis; therapeutic.

XX

OS Homo sapiens.

XX

PN W09428931-A1.

XX

PD 22-DEC-1994.

XX

PF 07-JUN-1994; 94WO-US006380.

XX

PR 11-JUN-1993; 93US-00076093.

XX

PA (GETH) GENENTECH INC.

XX

PI Chuntharapai A, Lee J, Hebert C, Kim KJ;

XX

DR WPI; 1995-036114/05.

DR N-PSDB; AAQ80521.
 XX
 PT Treatment of inflammatory disorders - by administering an antibody
 PT capable of binding a platelet factor 4 superfamily receptor polypeptide.
 XX
 PS Disclosure; Page 54-56; 83pp; English.
 XX
 CC 2 PF4AR members were identified by probing lambda libraries from human
 CC monoclyte-like cell line HL-60 and human peripheral blood lymphocytes
 CC using a large fragment of IL-8 receptor DNA (full sequence given in
 CC AAQ80520). The nucleotide sequences of the 2 PF4ARs are given in AAQ80521
 CC and AAQ80522, and their respective amino acid sequences in AAR68812 and
 CC AAR68813. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
 |||
 Db 1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
 Qy 61 LVMGYQKKLRSMIDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
 |||
 Db 61 LVMGYQKKLRSMIDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
 Qy 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 |||
 Db 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 Qy 181 DDRIYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
 |||
 Db 181 DDRIYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
 Qy 241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
 |||
 Db 241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
 Qy 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
 |||
 Db 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352

RESULT 2

AAR80757

ID AAR80757 standard; protein; 352 AA.

XX

AC AAR80757;

XX

DT 25-MAR-2003 (revised)

DT 26-MAR-1996 (first entry)

XX

DE Chemokine superfamily receptor.

XX

KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;

KW rheumatoid arthritis; inflammatory bowel disease;

KW chronic lung inflammation; treatment; antibody; affinity purification;
 KW detection.

XX

OS Homo sapiens.

XX

PN US5440021-A.

XX

PD 08-AUG-1995.

XX

PF 25-FEB-1994; 94US-00202056.

XX

PR 29-MAR-1991; 91US-00677211.

XX

PA (HEBE/) HEBERT C.

PA (CHUN/) CHUNTHARAPAI A.

PA (KIMK/) KIM K J.

PA (LEEJ/) LEE J.

XX

PI Chuntharapai A, Kim KJ, Hebert C, Lee J;
 XX
 DR WPI; 1995-283151/37.
 DR N-PSDB; AAQ99007.
 XX
 PT New antibodies against interleukin 8 type B receptor - used to treat or
 PT prevent inflammation, also for detecting receptor expression and
 PT purificn.
 XX
 PS Example 2; Col 45-48; 62pp; English.
 XX
 CC Antibodies directed against the interleukin-8 receptor B can be used to
 CC treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid
 CC arthritis and particularly inflammatory bowel disease and chronic lung
 CC inflammation. When immobilised, these antibodies may be used to detect
 CC interleukin-8 receptor B expression in cells and tissues and for affinity
 CC purification of interleukin-8 receptor B from cells. This sequence is an
 CC additional chemokine superfamily receptor which was identified by probing
 CC lamda libraries of genomic DNA from a human monocyte-like cell line (L-
 CC 60) and human peripheral blood lymphocytes using a large fragment of the
 CC interleukin-8 type A receptor DNA (See AAQ99006). (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEGISIIYTSNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYTSNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCI IISKLSHSGKHQKRKALKT 240
        |||
Db    181 DDRYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCI IISKLSHSGKHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 3

AA39993

ID AAY39993 standard; protein; 352 AA.

XX

AC AAY39993;

XX

DT 16-DEC-1999 (first entry)

XX

DE Human CXCR4 protein sequence.

XX

KW CXCR4; human; neovascularisation; inhibitor; solid cancer; therapy;

KW tissue repairing agent; vascularisation.

XX

OS Homo sapiens.

XX

PN W09948528-A1.

XX

PD 30-SEP-1999.

XX

PF 23-MAR-1999; 99WO-JP001448.

XX

PR 24-MAR-1998; 98JP-00095448.

XX
PA (CHUS) CHUGAI SEIYAKU KK.
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T, Nagasawa T, Tachibana K;
XX
DR WPI; 1999-591042/50.
DR N-PSDB; AAZ27610.
XX
PT CXCR4-potentiating agents and methods useful for inhibiting
PT neovascularization, and treating solid cancers.
XX
PS Disclosure; Page 47-48; 63pp; Japanese.
XX
CC This sequence is the human CXCR4 protein. The invention relates to
CC remedies inhibiting neovascularisation, remedies for solid cancer,
CC remedies for diseases pathologically caused by neovascularisation and
CC tissue repairing agents containing as the active ingredient a substance
CC capable of potentiating CXCR4. Based on a finding that vascularisation is
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
CC remedies inhibiting vascularisation which contain as the active
CC ingredient a substance capable of potentiating CXCR4, remedies for solid
CC cancer, remedies for diseases pathologically caused by neovascularisation
CC and tissue repairing agents containing as the active ingredient a
CC substance capable of potentiating CXCR4. It is also possible to establish
CC methods for treatment with the use of these remedies
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
          |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
          |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
          |||
Db    121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKALKT 240
          |||
Db    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
          |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
          |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 4

AA52507

ID AAY52507 standard; protein; 352 AA.

XX

AC AAY52507;

XX

DT 22-FEB-2000 (first entry)

XX

DE Human CXC-chemokine receptor-4 (CXCR-4).

XX

KW CXC-chemokine receptor-4; CXCR-4; stromal cell derived factor-1; SDF-1;
KW ligand; chemotaxis; inflammation; G-protein-coupled receptor;
KW signal transduction; CD4-independent; HIV-1; infection; proliferation;
KW transformation; tumorigenesis; cancer; tumour; overexpression; brain;
KW breast; colon; lung; melanoma; glioblastoma; inhibition; growth arrest;
KW diagnosis; prognosis; marker; proliferative disorders; antisense;
KW therapy; treatment; premalignant condition; hypertrophy;
KW degenerative disorder; Parkinson's disease; Alzheimer's disease;

KW growth deficiency; hypoproliferative disorder; physical trauma; lesion;
 KW ischaemia; wound.
 XX
 OS Homo sapiens.
 XX
 PN WO9950461-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 29-MAR-1999; 99WO-US007431.
 XX
 PR 30-MAR-1998; 98US-0079916P.
 PR 16-OCT-1998; 98US-0104656P.
 XX
 PA (NWBI-) NORTHWEST BIOTHERAPEUTICS INC.
 XX
 PI Murphy GP, Boynton AL, Sehgal A;
 XX
 DR WPI; 2000-052634/04.
 DR N-PSDB; AAZ38553.
 XX
 PT Use of CXCR-4 and SDF-1 as markers for diagnosis and treatment of e.g.
 PT tumors, degenerative disorders, growth deficiencies, hyper- and
 PT hypoproliferative disorders, physical trauma, lesions and wounds.
 XX
 PS Disclosure; Fig 14; 138pp; English.
 XX
 CC This sequence represents CXC-chemokine receptor-4 (CXCR-4). Chemokine
 CC receptors play an important role in the chemotaxis of T-cells and
 CC phagocytic cells to areas of inflammation. CXCR-4 is a member of the G-
 CC protein-coupled receptor family, which is involved in signal
 CC transduction, and its ligand is stromal cell derived factor-1 (SDF-1,
 CC AAY52508). CXCR-4 also mediates CD4-independent infection by HIV-1. CXCR-
 CC 4 has now been found to have a role in the aberrant proliferative
 CC behaviour of a number of cell types, including numerous primary tumours
 CC and derived cell lines. CXCR-4 is involved in cell transformation and
 CC tumorigenesis, particularly in brain, breast and colon tumours. It was
 CC found to be overexpressed in several brain tumour derived cell lines and
 CC primary brain tumour tissues, breast tumour tissues, colorectal
 CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression
 CC was required for the continuous proliferation of glioblastoma cancer
 CC cells, and inhibition of its gene function resulted in growth arrest.
 CC Conversely, overexpression resulted in enhanced and rapid cellular
 CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis
 CC and prognosis of cell proliferative disorders, and antisense
 CC oligonucleotides complementary to at least a portion of an RNA transcript
 CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour
 CC cell. Agents that inhibit CXCR-4 function can be used for treating or
 CC preventing a disease or disorder involving cell overproliferation, e.g.,
 CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell
 CC lymphoma, and also premalignant conditions, benign tumours,
 CC hyperproliferative disorders, and benign dysproliferative disorders. They
 CC can also be used for treating e.g., cirrhosis of the liver, keloid
 CC formation, psoriasis, benign tumors, fibrocystic conditions and tissue
 CC hypertrophy. Compounds that promote CXCR-4 function can also be used for
 CC preventing or treating a disease or disorder involving a deficiency in
 CC cell proliferation, or treating a condition where cell proliferation
 CC would be desirable. Such diseases include degenerative disorders (e.g.,
 CC Parkinson's disease, Alzheimer's disease), growth deficiencies,
 CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused
 CC by ischaemia), and wounds
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
         |||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         |||||||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
```

Qy 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 |||||
 Db 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
 |||||
 Qy 181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
 |||||
 Db 181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
 |||||
 Qy 241 TVILILAFFACWLPPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
 |||||
 Db 241 TVILILAFFACWLPPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
 |||||
 Qy 301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
 |||||
 Db 301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
 |||||

RESULT 5

AAE06690

ID AAE06690 standard; protein; 352 AA.

XX

AC AAE06690;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human neuropeptide Y (NPY) Y3 receptor.

XX

KW Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
 KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
 KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
 KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
 KW NPY Y3 receptor.

XX

OS Homo sapiens.

XX

PN WO200153477-A1.

XX

PD 26-JUL-2001.

XX

PF 22-JAN-2001; 2001WO-US002040.

XX

PR 20-JAN-2000; 2000US-00489872.

XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PA (AMLI/) AMLING M.

XX

PI Amling M, Karsenty G, Ducey P;

XX

DR WPI; 2001-488709/53.

DR N-PSDB; AAD12801.

XX

PT Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
 PT the level of neuropeptide Y activity in blood or cerebrospinal fluid.

XX

PS Example 7; Page 85; 102pp; English.

XX

CC The present invention relates to a method for treatment or prevention of
 CC bone diseases characterised by loss of bone mass, comprises administering
 CC to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
 CC the serum or cerebrospinal fluid (CSF) or a compound that lowers the
 CC level of inositol phosphate (IP) or extracellular signal-regulated kinase
 CC (ERK). The method is specifically used to treat (including by gene
 CC therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
 CC also be used e.g., in cases of fractures or bone metastases. These
 CC diseases may also be diagnosed by detecting elevated NPY levels,
 CC including monitoring of treatment, assessing efficacy of compounds in
 CC clinical trials and for identifying subjects at risk. The present
 CC sequence is a human NPY Y3 receptor

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.7e-213;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGISIIYTSNYTEEMSGDYDSMKPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

```

Db      1 MEGISIIYTS DNYTEEMSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
Qy      61 LVMGYQKKLRSM TDK YRLHLSVADLLFVITLPFWAVDAVANWYFGN FLCKAVHVIYTVNL 120
Db      61 LVMGYQKKLRSM TDK YRLHLSVADLLFVITLPFWAVDAVANWYFGN FLCKAVHVIYTVNL 120
Qy      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180
Db      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180
Qy      181 D DRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGHQKRKALKT 240
Db      181 D DRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGHQKRKALKT 240
Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
Qy      301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
Db      301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 6
AAG79088

ID. AAG79088 standard; protein; 352 AA.

XX

AC AAG79088;

XX

DT 10-DEC-2001 (first entry)

XX

DE Amino acid sequence of human CXCR4 protein.

XX

KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;

KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection;

KW CXCR4.

XX

OS Homo sapiens.

XX

PN WO200164752-A2.

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US006322.

XX

PR 02-MAR-2000; 2000US-00517605.

XX

PA (UYN Y) UNIV NEW YORK STATE.

PA (UYN I-) UNIV NIJMEGEN.

XX

PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;

XX

DR WPI; 2001-602565/68.

XX

PT An antibody for the treatment or prevention of HIV-infection comprises a

PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of

PT DC-SIGN due to concomitant conformational change.

XX

PS Disclosure; Page 117-118; 131pp; English.

XX

CC The specification describes an antibody which is specific for an
CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
CC is exposed upon gp120 binding of DC-SIGN due to concomitant
CC conformational change. DC-SIGN is a receptor that is specifically
CC expressed on dendritic cells and facilitates infection of T lymphocytes
CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
CC with high affinity. The antibody of the invention inhibits the trans
CC enhancement of HIV entry into a T cell or macrophage facilitated by
CC dendritic cells. The antibody is useful to treat or prevent HIV
CC infection. The present sequence represents a human CXCR4 protein, which
CC is a translocation promoting agent that interacts with CD4. This receptor
CC functions in HIV-1 entry into cells

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
        |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 D DRYICDRFY PNDLWVVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGHQKRKALKT 240
        |||
Db    181 D DRYICDRFY PNDLWVVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGHQKRKALKT 240

Qy    241 TVILILAFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 7

AAG80123

ID AAG80123 standard; protein; 352 AA.

XX

AC AAG80123;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CXCR4 protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN W0200172830-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP003708.

XX

PR 31-MAR-2000; 2000DE-01016013.

XX

PA (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSSMANN U.

XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX

DR WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.

XX

PS Disclosure; Page 12; 26pp; German.

XX

CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),

CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEGISIIYSDNYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYSDNYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFPNDLWVVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGKHQKRKALKT 240
        |||
Db    181 DDRYICDRFPNDLWVVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGKHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
  
```

RESULT 8

AAO14003

ID AAO14003 standard; protein; 352 AA.

XX

AC AAO14003;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human cysteine-X-cysteine chemokine receptor 4.

XX

KW Cysteine-X-Cysteine Chemokine Receptor 4; CXCR4 binding peptide;

KW chemoattractant cytokine; human immunodeficiency virus; HIV;

KW HIV envelope glycoprotein; cellular CD4 receptor; env gene; gp160; gp120;

KW gp41; CD4+ target cell; HIV-infected cell; CXCR4-binding compound;

KW acquired immunodeficiency syndrome; AIDS; human; receptor.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .39

FT /note= "Extracellular N-terminus; this is involved in HIV
 entry into a cell"

FT Region 40. .64

FT /note= "Transmembrane segment 1 (TM1)"

FT Region 65. .76

FT /note= "Intracellular loop 1"

FT Region 77. .99

FT /note= "Transmembrane segment 2 (TM2)"

FT Region 100. .110

FT /note= "Extracellular loop 1"

FT Region 111. .131

FT /note= "Transmembrane segment 3 (TM3)"

FT Region 132. .176

FT /note= "Intracellular loop 2"

FT Region 177. .197

FT /note= "Transmembrane segment 4 (TM4)"
 FT Region 198. .203
 FT /note= "Extracellular loop 2; required for HIV entry into
 FT a cell"
 FT Region 204. .223
 FT /note= "Transmembrane segment 5 (TM5)"
 FT Region 224. .240
 FT /note= "Intracellular loop 3"
 FT Region 241. .261
 FT /note= "Transmembrane segment 6 (TM6)"
 FT Region 262. .282
 FT /note= "Extracellular loop 3; this is involved in HIV
 FT entry into a cell"
 FT Binding-site 275
 FT /note= "Binds HIV gp120"
 FT Binding-site 278
 FT /note= "Binds HIV gp120"
 FT Misc-difference 280. .281
 FT /note= "Apparently encoded by nucleotides 838-903 of
 FT AAK98241"
 FT Region 283. .307
 FT /note= "Transmembrane segment 7 (TM7)"
 FT Region 308. .352
 FT /note= "Intracellular C-terminus"
 XX

PN WO200170768-A2.

XX

PD 27-SEP-2001.

XX

PF 21-MAR-2001; 2001WO-US009160.

XX

PR 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.

PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX

PA (CONS-) CONSENSUS PHARM INC.

XX

PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA;

XX

DR WPI; 2002-010593/01.

DR N-PSDB; AAK98241.

XX

PT Identifying agents that bind to CXC chemokine receptor 4, useful for
 PT treatment and prevention of acquired immunodeficiency syndrome, comprises
 PT screening compound library for members that bind to the receptor.
 XX

PS Example 3; Fig 3B; 46pp; English.

XX

CC The invention relates to a method of identifying Cysteine-X-Cysteine
 CC chemokine receptor 4 (CXCR4) binding compounds. The method comprises
 CC testing and selecting compounds in a library for their ability to bind to
 CC CXCR4. Chemokines (chemoattractant cytokines) regulate the movement and
 CC biological activities of leukocytes in many disease situations. CXCR4
 CC acts as a co-receptor for human immunodeficiency virus (HIV), as it
 CC interacts with the HIV envelope glycoproteins and the cellular CD4
 CC receptor, to facilitate HIV entry into cells. The HIV glycoproteins
 CC (encoded by the env gene) are translated as a precursor (gp160) which is
 CC subsequently cleaved into gp120 and gp41. Gp120 binds to CXCR4 and the
 CC CD4 receptor present on the surface of susceptible CD4+ target cells,
 CC causing the virus to fuse with the cell membranes and thereby
 CC facilitating entry of the virus into the cell. The eventual expression of
 CC the env product on the surface of the HIV-infected cell enables the cell
 CC to fuse with uninfected CD4+ cells, thereby spreading the infection. The
 CC CXCR4-binding compounds of the invention inhibit the entry of HIV into
 CC the CD4+ cell and therefore are useful in the prevention of HIV infection
 CC and the treatment and prevention of acquired immunodeficiency syndrome
 CC (AIDS). The present sequence represents the human CXCR4 protein used in
 CC the method of the invention
 XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MEGISIIYTSQNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYTSQNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

QY     61 LVMGYQKKLRSMQDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVMGYQKKLRSMQDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

QY    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

QY    181 DDRYICDRFYPNDLWVVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DDRYICDRFYPNDLWVVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

QY    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

QY    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
```

RESULT 9

ABP52651

ID ABP52651 standard; protein; 352 AA.

XX

AC ABP52651;

XX

DT 30-OCT-2002 (first entry)

XX

DE Human CXC chemokine receptor 4 protein SEQ ID NO:126.

XX

KW Cysteine-X-cysteine chemokine receptor 4; CXC chemokine receptor 4;

KW binding; identification; AIDS; HIV; CXCR4; virucide; anti-HIV.

XX

OS Homo sapiens.

XX

PN W0200257313-A2.

XX

PD 25-JUL-2002.

XX

PF 26-OCT-2001; 2001WO-US051165.

XX

PR 27-OCT-2000; 2000US-0243587P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX

PA (CONS-) CONSENSUS PHARM INC.

XX

PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA, Krstenansky J;

XX

DR WPI; 2002-608378/65.

DR N-PSDB; ABQ74938.

XX

PT Identifying a binding compound for cysteine-X-cysteine chemokine receptor

PT 4 (CXCR4) for preventing or treating AIDS and HIV infection, comprises

PT binding a molecule to a molecule with a binding property corresponding to

PT CXCR4.

XX

PS Example 3; Fig 3A-B; 92pp; English.

XX

CC The present invention describes a method (M1) for identifying a binding

CC compound for cysteine-X-cysteine chemokine receptor 4 (CXCR4) comprises

CC binding a molecule from the library of two or more molecules to the

CC molecule with a binding property corresponding to CXCR4. (M1) comprises:

CC (a) providing a library of two or more molecules; (b) providing a

CC molecule with a binding property corresponding to CXCR4; (c) binding a

CC molecule from the library of two or more molecules to the molecule with a

CC binding property corresponding to CXCR4; (d) separating the bound

CC molecule from the library of two or more molecules; and (e) identifying

CC the bound molecule as a binding compound for CXCR4. Also described is a
 CC binding compound (I) for CXCR4 identified from M1. (I) has virucide and
 CC anti-HIV activities. A partially purified CXCR4 protein is useful for
 CC carrying out selection, identification and improvement of tight binding
 CC ligands in identifying therapeutically useful compounds. Therapeutic
 CC peptides, peptidomimetics, or small molecule antagonists or agonists of
 CC CXCR4 binding may be used in the prevention and treatment of AIDS and HIV
 CC infection. The present sequence represents human CXCR4 which is given in
 CC an example from the present invention

XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.7e-213;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMK EPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMK EPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVVGWVIPALLLTIPDFIFANVSEA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVVGWVIPALLLTIPDFIFANVSEA 180

Qy    181 D DRYICDRFYPN DLWVVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 D DRYICDRFYPN DLWVVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240

Qy    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 10

ABG32977

ID ABG32977 standard; protein; 352 AA.

XX

AC ABG32977;

XX

DT 02-DEC-2002 (first entry)

XX

DE Human CXC chemokine receptor 4 (CXCR4).

XX

KW CXC chemokine receptor 4; CXCR4; chemotaxis induction; SDF1a;
 KW stromal cell-derived factor 1alpha; angiogenesis; atherosclerosis;
 KW restenosis; ischaemic stroke; spinal cord injury; infection; ulcer;
 KW human immunodeficiency virus; HIV; acquired immunodeficiency syndrome;
 KW AIDS; pain; cancer; benign prostatic hypertrophy; diabetes; obesity;
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; stroke;
 KW anginal pectoris; myocardial infarction; benign prostatic hypertrophy;
 KW migraine; vomiting; psychotic disorder; neurological disorder; anxiety;
 KW schizophrenia; dyskinesia; Huntington's disease; restenosis;
 KW inflammatory disease; rheumatoid arthritis; diabetic retinopathy;
 KW inflammatory bowel disease; atherosclerosis; Alzheimer's disease;
 KW congestive heart failure; cardiac remodeling; angiogenic diseases;
 KW solid tumour; Kaposi Sarcoma; human.

XX

OS Homo sapiens.

XX

PN US2002107195-A1.

XX

PD 08-AUG-2002.

XX

PF 17-SEP-2001; 2001US-00953692.

XX

PR 21-JUL-1998; 98US-0093596P.

PR 21-JUL-1999; 99US-00358624.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Gupta SK;
XX
DR WPI; 2002-697879/75.
DR N-PSDB; ABS53992.
XX
PT Inducing chemotaxis of endothelial cells, useful for regulating
PT angiogenesis, e.g.. for treating cancer, comprises treatment with stromal
PT cell-derived factor 1 alpha.
XX
PS Claim 3; Fig 1; 26pp; English.
XX
CC The invention describes a method of inducing chemotaxis of endothelial
CC cells by treatment with stromal cell-derived factor 1alpha (SDF1a). The
CC method is used for stimulating EC chemotaxis, and thus angiogenesis, and
CC is used for treating atherosclerosis, restenosis, ischaemic stroke and
CC spinal cord injury. Inhibition of this process is useful in treatment and
CC prevention of a very wide range of diseases, such as, infection (by
CC bacteria, fungi, protozoa or viruses such as human immunodeficiency virus
CC (HIV) and acquired immunodeficiency syndrome (AIDS)), pain, cancer and
CC benign prostatic hypertrophy, diabetes, obesity, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, anginal pectoris,
CC myocardial infarction, stroke, ulcers, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia) and dyskinesias (e.g. Huntingdon's disease), inflammatory
CC diseases, rheumatoid arthritis, diabetic retinopathy, inflammatory bowel
CC disease, atherosclerosis, restenosis, Alzheimer's disease, congestive
CC heart failure, cardiac remodeling, angiogenic diseases, solid tumours,
CC and Kaposi Sarcoma. This is the amino acid sequence of a CXC chemokine

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074020_us-10-785-230-1.rup.

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[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074020_us-10-785-230-1.rup.

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GenCore version 6.2
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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:08:15 ; Search time 227 Seconds
(without alignments)
1660.742 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIIYTSNDNYTEEMGSGD.....KRGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0., Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	CXCR4_HUMAN	P61073 homo sapien
2	1830	100.0	352	1	CXCR4_PANTR	P61072 pan troglod
3	1830	100.0	352	2	Q53S69_HUMAN	Q53s69 homo sapien
4	1822	99.6	352	2	Q9BXA0_HUMAN	Q9bxa0 homo sapien
5	1813	99.1	352	1	CXCR4_PAPAN	P56491 papio anubi
6	1809	98.9	352	2	Q8HZU0_SAIISC	Q8hzu0 saimiri sci
7	1806	98.7	352	1	CXCR4_MACFA	Q28474 macaca fasc
8	1806	98.7	352	2	O77488_CERAE	O77488 cercopithec
9	1805	98.6	352	2	Q8HZU1_CALJA	Q8hzu1 callithrix
10	1803	98.5	352	1	CXCR4_MACMU	P79394 macaca mula
11	1803	98.5	352	2	Q9TSQ8_CERAE	Q9tsq8 cercopithec
12	1802	98.5	347	2	Q9MZN2_PONPY	Q9mzn2 pongo pygma
13	1802	98.5	347	2	Q9MZN1_9PRIM	Q9mzn1 gorilla gor
14	1802	98.5	347	2	Q9MZN6_HYLLE	Q9mzn6 nomascus le

15	1802	98.5	347	2	Q9MZN5_BUNHO	Q9mzn5 bunopithec
16	1799	98.3	352	2	Q9BDS5_MACFA	Q9bds5 macaca fasc
17	1798	98.3	347	2	Q9MZN4_HYLLA	Q9mzn4 hylobates l
18	1798	98.3	352	2	Q7YS92_9EUTH	Q7ys92 tupaia chin
19	1795	98.1	352	1	CXCR4_CERTO	O62747 cercocebus
20	1792	97.9	347	2	Q9MZN3_HYLSY	Q9mzn3 hylobates s
21	1786	97.6	347	2	Q9MZP5_9PRIM	Q9mzp5 presbytis p
22	1786	97.6	347	2	Q9MZP8_COLPO	Q9mzp8 colobus pol
23	1786	97.6	347	2	Q9MZQ2_PYGRO	Q9mzq2 pygathrix r
24	1786	97.6	347	2	Q9MZQ1_PYGBI	Q9mzq1 pygathrix b
25	1786	97.6	347	2	Q9MZP0_MACAS	Q9mzp0 macaca assa
26	1786	97.6	347	2	Q9MZN8_MACTH	Q9mzn8 macaca thib
27	1786	97.6	347	2	Q9MZN7_MACNE	Q9mzn7 macaca neme
28	1786	97.6	347	2	Q9MZP9_NASLA	Q9mzp9 nasalis lar
29	1786	97.6	347	2	Q9MZQ3_PYGAV	Q9mzq3 pygathrix a
30	1786	97.6	347	2	Q9MZQ0_PYGNE	Q9mzq0 pygathrix n
31	1786	97.6	347	2	Q9MZP4_PREFR	Q9mzp4 presbytis f
32	1786	97.6	347	2	Q9MZN9_MACAR	Q9mzn9 macaca arct
33	1782	97.4	347	2	Q9MZP7_9PRIM	Q9mzp7 presbytis s
34	1782	97.4	347	2	Q9MZP2_MANSP	Q9mzp2 mandrillus
35	1781	97.3	347	2	Q9MZM9_ATEPA	Q9mzm9 ateles pani
36	1779	97.2	347	2	Q9MZN5_PITPI	Q9mzm5 pithecia pi
37	1779	97.2	347	2	Q9MZN7_CALGO	Q9mzm7 callimico g
38	1778	97.2	347	2	Q9MZP6_9PRIM	Q9mzp6 presbytis j
39	1778	97.2	347	2	Q9MZP3_SEMEN	Q9mzp3 semnopithec
40	1777	97.1	347	2	Q9MZN0_ALOSE	Q9mzn0 alouatta se
41	1771	96.8	347	2	Q9MZP1_MANLE	Q9mzp1 mandrillus
42	1771	96.8	347	2	Q9MZM6_CALMO	Q9mzm6 callicebus
43	1760	96.2	347	2	Q9MZM8_CALJA	Q9mzm8 callithrix
44	1754.5	95.9	353	2	Q3LSL6_CANFA	Q3ls16 canis famil
45	1754	95.8	347	2	Q9MZM1_EULMA	Q9mzm1 eulemur mac

ALIGNMENTS

RESULT 1

CXCR4_HUMAN

ID CXCR4_HUMAN STANDARD; PRT; 352 AA.
AC P61073; O60835; P30991; P56438; Q9UKN2;
DT 26-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT 26-APR-2004, sequence version 1.
DT 13-JUN-2006, entry version 27.
DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE seven transmembrane domain receptor) (LESTR) (LCR1) (FB22) (NPYRL)
DE (HM89) (CD184 antigen).
GN Name=CXCR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION.
RC TISSUE=Lung;
RX MEDLINE=93319629; PubMed=8329116;
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT "Molecular cloning, characterization, and localization of the human
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
RT and activation.";
RL DNA Cell Biol. 12:465-471(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION.
RC TISSUE=Fetal brain;
RX MEDLINE=94052833; PubMed=8234909; DOI=10.1016/0167-0115(93)90392-L;
RA Jazin E.E., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker M.W.,
RA Salon J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC TISSUE=Fetal spleen;
RX MEDLINE=93315164; PubMed=8325644;

RA Federspiel B., Melhado I.G., Duncan A.M., Delaney A.D.,
 RA Schappert K.T., Clark-Lewis I., Jirik F.R.;
 RT "Molecular cloning of the cDNA and chromosomal localization of the
 RT gene for a putative seven-transmembrane segment (7-TMS) receptor
 RT isolated from human spleen.";
 RL Genomics 16:707-712(1993).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RC TISSUE=Monocyte;
 RX MEDLINE=94103215; PubMed=8276799;
 RA Loetscher M., Geiser T., O'Reilly T., Zwahlen R., Baggiolini M.,
 RA Moser B.;
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
 RT is highly expressed in leukocytes.";
 RL J. Biol. Chem. 269:232-237(1994).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND CHARACTERIZATION OF ITS
 RP HIV-1 CORECEPTOR FUNCTION.
 RX MEDLINE=96217947; PubMed=8629022;
 RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
 RT "HIV-1 entry cofactor: functional cDNA cloning of a seven-
 RT transmembrane, G protein-coupled receptor.";
 RL Science 272:872-877(1996).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC TISSUE=Peripheral blood leukocyte;
 RX MEDLINE=98136183; PubMed=9468539; DOI=10.1074/jbc.273.8.4754;
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Sleeker A.L.,
 RA Michael N.L.;
 RT "Genomic organization and functional characterization of the chemokine
 RT receptor CXCR4, a major entry co-receptor for human immunodeficiency
 RT virus type 1.";
 RL J. Biol. Chem. 273:4754-4760(1998).
 RN [8]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=98258970; PubMed=9599023; DOI=10.1016/S0014-5793(98)00359-7;
 RA Caruz A., Sansom M., Alonso J.M., Alcamí J., Baleux F.,
 RA Virelizier J.-L., Parmentier M., Arenzana-Seisdedos F.;
 RT "Genomic organization and promoter characterization of human CXCR4
 RT gene.";
 RL FEBS Lett. 426:271-278(1998).
 RN [9]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RX MEDLINE=99408510; PubMed=10480633; DOI=10.1089/088922299310296;
 RA Xiao L., Weiss S.H., Qari S.H., Rudolph D., Zhao C., Denny T.N.,
 RA Hodge T., Lal R.B.;
 RT "Partial resistance to infection by R5X4 primary HIV type 1 isolates
 RT in an exposed-uninfected individual homozygous for CCR5 32-base pair
 RT deletion.";
 RL AIDS Res. Hum. Retroviruses 15:1201-1208(1999).
 RN [10]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC TISSUE=Peripheral blood lymphocyte;
 RX MEDLINE=99095114; PubMed=9879064;
 RA Frodl R., Gierschik P., Moepps B.;
 RT "Genomic organization and expression of the CXCR4 gene in mouse and
 RT man: absence of a splice variant corresponding to mouse CXCR4-B in
 RT human tissues.";
 RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
 RN [11]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RC TISSUE=Neutrophil;
 RX MEDLINE=99384048; PubMed=10452968;
 RA Gupta S.K., Pillarisetti K.;
 RT "CXCR4-Lo: molecular cloning and functional expression of a novel
 RT human CXCR4 splice variant.";
 RL J. Immunol. 163:2368-2372(1999).
 RN [12]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC TISSUE=Lung;
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [13]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [14]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [16]
RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882; DOI=10.1016/S0092-8674(00)80577-2;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry.";
RL Cell 96:667-676(1999).
RN [17]
RP FUNCTION.
RX MEDLINE=96351077; PubMed=8752280; DOI=10.1038/382829a0;
RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
RA Sodroski J., Springer T.A.;
RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
RT blocks HIV-1 entry.";
RL Nature 382:829-833(1996).
RN [18]
RP FUNCTION.
RX MEDLINE=96351078; PubMed=8752281; DOI=10.1038/382833a0;
RA Oberlin E., Amara A., Bachelier F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RT "The CXCR chemokine SDF-1 is the ligand for LESTR/fusin and prevents
RT infection by T-cell-line-adapted HIV-1.";
RL Nature 382:833-835(1996).
RN [19]
RP ERRATUM.
RA Oberlin E., Amara A., Bachelier F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RL Nature 384:288-288(1996).
RN [20]

RP CHARACTERIZATION AS HIV-1 CORECEPTOR.
 RX MEDLINE=97002453; PubMed=8849450; DOI=10.1126/science.274.5287.602;
 RA Lapham C.K., Ouyang J., Chandrasekhar B., Nguyen N.Y., Dimitrov D.S.,
 RA Golding H.;
 RT "Evidence for cell-surface association between fusin and the CD4-gp120
 RT complex in human cell lines.";
 RL Science 274:602-605(1996).
 RN [21]
 RP CHARACTERIZATION AS HIV-2 PRIMARY RECEPTOR IN SOME ISOLATES.
 RX MEDLINE=97083584; PubMed=8929542; DOI=10.1016/S0092-8674(00)81393-8;

Query Match 100.0%; Score 1830; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.5e-133;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

CXCR4_PANTR

ID CXCR4_PANTR STANDARD; PRT; 352 AA.
 AC P61072; O60835; P30991; P56438; Q9UKN2;
 DT 26-APR-2004, integrated into UniProtKB/Swiss-Prot.
 DT 26-APR-2004, sequence version 1.
 DT 18-APR-2006, entry version 19.
 DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
 GN Name=CXCR4;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A.C., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 CC -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- PTM: Sulfated (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U89798; AAC03718.1; -; mRNA.
 DR InterPro; IPR000355; Chm_kine_rcpt.
 DR InterPro; IPR001277; CXC_4_rcpt.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00657; CCCHEMOKINER.
 DR PRINTS; PR00645; CXCCHMKINER4.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
 KW Sulfation; Transducer; Transmembrane.
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 FT /FTId=PRO_0000069356.
 FT TOPO_DOM 1 39 Extracellular (Potential).
 FT TRANSMEM 40 63 1 (Potential).
 FT TOPO_DOM 64 79 Cytoplasmic (Potential).
 FT TRANSMEM 80 99 2 (Potential).
 FT TOPO_DOM 100 110 Extracellular (Potential).
 FT TRANSMEM 111 132 3 (Potential).
 FT TOPO_DOM 133 154 Cytoplasmic (Potential).
 FT TRANSMEM 155 175 4 (Potential).
 FT TOPO_DOM 176 200 Extracellular (Potential).
 FT TRANSMEM 201 220 5 (Potential).
 FT TOPO_DOM 221 240 Cytoplasmic (Potential).
 FT TRANSMEM 241 261 6 (Potential).
 FT TOPO_DOM 262 285 Extracellular (Potential).
 FT TRANSMEM 286 305 7 (Potential).
 FT TOPO_DOM 306 352 Cytoplasmic (Potential).
 FT MOD_RES 21 21 Sulfotyrosine (Potential).
 FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
 FT DISULFID 109 186 By similarity.
 SQ SEQUENCE 352 AA; 39746 MW; 8C8476A186786B83 CRC64;

Query Match 100.0%; Score 1830; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.5e-133;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMK EPCFREENANFNKIFLPTIYSIIFLT GIVGNGLVI 60
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RESULT 3
 Q53S69_HUMAN
 ID Q53S69_HUMAN PRELIMINARY; PRT; 352 AA.
 AC Q53S69;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 13-JUN-2006, entry version 13.
 DE Hypothetical protein CXCR4.
 GN Name=CXCR4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Abbott A., Lamar B., Ureta M.;
 RT "The sequence of Homo sapiens BAC clone RP11-809C23.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL; AC068492; AAY24044.1; -; Genomic_DNA.
 DR UniGene; Hs.421986; -.
 DR Ensembl; ENSG00000121966; Homo sapiens.
 DR RZPD-ProtExp; A0419; -.
 DR RZPD-ProtExp; RZPD0834F0245; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000355; Chmkine_rcpt.
 DR InterPro; IPR001277; CXC_4_rcpt.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR00645; CXCCHMKINER4.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Hypothetical protein; Membrane; Receptor;
 KW Transducer; Transmembrane.
 SQ SEQUENCE 352 AA; 39746 MW; 8C8476A186786B83 CRC64;

Query Match 100.0%; Score 1830; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.5e-133;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLNPI 300
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Db    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352
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RESULT 4
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ID Q9BXA0_HUMAN PRELIMINARY; PRT; 352 AA.
AC Q9BXA0;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 13-JUN-2006, entry version 25.
DE Chemokine receptor CXCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fan Z., Li T., Li J., Luo B.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF348491; AAK29630.1; -; mRNA.
DR Ensembl; ENSG00000121966; Homo sapiens.
DR RZPD-ProtExp; A0419; -.
DR RZPD-ProtExp; RZPD0834F0245; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000355; Chmkine_rcpt.
DR InterPro; IPR001277; CXC_4_rcpt.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00657; CCCHEMOKINER.
DR PRINTS; PR00645; CXCCHMKINER4.
DR PRINTS; PR00237; GPCRHRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 352 AA; 39743 MW; 0A5F0E4210C81469 CRC64;

Query Match 99.6%; Score 1822; DB 2; Length 352;
Best Local Similarity 99.4%; Pred. No. 2.7e-132;
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Qy    121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
         |||
Db    121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240
         |||
Db    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLNPI 300
         |||
Db    241 TIIPILAFFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
         |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 5

CXCR4_PAPAN
ID CXCR4_PAPAN STANDARD; PRT; 352 AA.
AC P56491;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DT 18-APR-2006, entry version 33.
DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
GN Name=CXCR4;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98346785; PubMed=9683255; DOI=10.1016/S0161-5890(98)00016-9;
RA Benton P.A., Lee D.R., Kennedy R.C.;
RT "Sequence comparisons of non-human primate HIV-1 coreceptor
RT homologues."
RL Mol. Immunol. 35:95-101(1998).
CC -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC Transduces a signal by increasing the intracellular calcium ions
CC level (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- PTM: Sulfated (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF031089; AAC63831.1; -; mRNA.
DR InterPro; IPR000355; Chmkine_rcpt.
DR InterPro; IPR001277; CXC_4_rcpt.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CXCHEMOKINER.
DR PRINTS; PR00645; CXCRMKINER4.
DR PRINTS; PR00237; GPCRHRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW Sulfation; Transducer; Transmembrane.
FT CHAIN 1 352 C-X-C chemokine receptor type 4.
FT /FTId=PRO_0000069357.
FT TOPO_DOM 1 39 Extracellular (Potential).
FT TRANSMEM 40 63 1 (Potential).
FT TOPO_DOM 64 79 Cytoplasmic (Potential).
FT TRANSMEM 80 99 2 (Potential).
FT TOPO_DOM 100 110 Extracellular (Potential).
FT TRANSMEM 111 132 3 (Potential).
FT TOPO_DOM 133 154 Cytoplasmic (Potential).
FT TRANSMEM 155 175 4 (Potential).
FT TOPO_DOM 176 200 Extracellular (Potential).
FT TRANSMEM 201 220 5 (Potential).
FT TOPO_DOM 221 240 Cytoplasmic (Potential).
FT TRANSMEM 241 261 6 (Potential).
FT TOPO_DOM 262 285 Extracellular (Potential).
FT TRANSMEM 286 305 7 (Potential).
FT TOPO_DOM 306 352 Cytoplasmic (Potential).
FT MOD_RES 21 21 Sulfotyrosine (Potential).
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT DISULFID 109 186 By similarity.
SQ SEQUENCE 352 AA; 39752 MW; 468E542E1851265A CRC64;

Query Match 99.1%; Score 1813; DB 1; Length 352;
Best Local Similarity 98.9%; Pred. No. 1.3e-131;
Matches 348; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGISIIYSDNYTEEMGSGDYDSMKPEPCFREANANFNKIFLPTIYSIIFLTGVGNGLVI 60
Db 1 MEGISIIYSDNYTEEMGSGDYDSIKEPCFREANAHFNRIPLPTIYSIIFLTGVGNGLVI 60

Qy 61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLFFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
Db 61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLFFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

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Qy      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFASVSEA 180

Qy      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352

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RESULT 6

Q8HZUO_SAISC

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ID  Q8HZUO_SAISC  PRELIMINARY;  PRT;  352 AA.
AC  Q8HZUO;
DT  01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT  01-MAR-2003, sequence version 1.
DT  30-MAY-2006, entry version 19.
DE  Chemokine receptor CXCR4.
OS  Saimiri sciureus (Common squirrel monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC  Platyrrhini; Cebidae; Saimiriinae; Saimiri.
OX  NCBI_TaxID=9521;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA  LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT  "Blockade of HIV-1 infection of New World monkey cells occurs
RT  primarily at the stage of virus entry.";
RL  J. Exp. Med. 196:431-445(2002).
CC  -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC  -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AF452613; AAN14529.1; -; mRNA.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR  GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR  GO; GO:0007165; P:signal transduction; IEA.
DR  InterPro; IPR000355; Chmkine_rcpt.
DR  InterPro; IPR001277; CXCR4_rcpt.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00657; CXCHEMOKINER.
DR  PRINTS; PR00645; CXCHEMOKINER4.
DR  PRINTS; PR00237; GPCR_RHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Membrane; Receptor; Transducer;
KW  Transmembrane.
SQ  SEQUENCE 352 AA; 39821 MW; BF1A21FB0C8D4487 CRC64;

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Query Match      98.9%;  Score 1809;  DB 2;  Length 352;
Best Local Similarity  98.6%;  Pred. No. 2.7e-131;
Matches 347;  Conservative  4;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy      1 MEGISIIYSDNYTEEMGSGDYDSMKPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYSDNYTEEMGSGDYDSMKPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      61 LVMGYQKKLRSMIDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNL 120
Qy      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
Qy      181 DDYRICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240
        |||
Db      181 DDYRICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240
Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPI 300
Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 7

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CXCR4_MACFA
ID   CXCR4_MACFA      STANDARD;          PRT;   352 AA.
AC   Q28474;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   18-APR-2006, entry version 35.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR) (CD184
DE   antigen).
GN   Name=CXCR4;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Tatsumi M., Takahashi H.;
RT   "Monkey CD4 and fusin are not species barrier for HIV-1 replication.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC   Transduces a signal by increasing the intracellular calcium ions
CC   level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; D86579; BAA13126.1; -; mRNA.
DR   PIR; G00048; G00048.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCR RHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN           1       352       C-X-C chemokine receptor type 4.
FT                                     /FTId=PRO_0000069353.
FT   TOPO_DOM        1       39       Extracellular (Potential).
FT   TRANSMEM        40      63       1 (Potential).
FT   TOPO_DOM        64      79       Cytoplasmic (Potential).
FT   TRANSMEM        80      99       2 (Potential).
FT   TOPO_DOM       100     110       Extracellular (Potential).
FT   TRANSMEM       111     132       3 (Potential).
FT   TOPO_DOM       133     154       Cytoplasmic (Potential).
FT   TRANSMEM       155     175       4 (Potential).
FT   TOPO_DOM       176     200       Extracellular (Potential).
FT   TRANSMEM       201     220       5 (Potential).
FT   TOPO_DOM       221     240       Cytoplasmic (Potential).

```

FT	TRANSMEM	241	261	6 (Potential).
FT	TOPO_DOM	262	285	Extracellular (Potential).
FT	TRANSMEM	286	305	7 (Potential).
FT	TOPO_DOM	306	352	Cytoplasmic (Potential).
FT	MOD_RES	21	21	Sulfotyrosine (Potential).
FT	CARBOHYD	11	11	N-linked (GlcNAc...) (Potential).
FT	DISULFID	109	186	By similarity.
SQ	SEQUENCE	352 AA;	39753 MW;	432DA6C11859EF8A CRC64;

Qy	1	MEGISIYTSNDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI	60
Db	1	MEGISIYTSNDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI	60
Qy	61	LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL	120
Db	61	LVMGYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL	120
Qy	121	YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKV VYGVWIPALLTIPDFIFANVSEA	180
Db	121	YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKV VYGVWIPALLTIPDFIFASVSEA	180
Qy	181	DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSKGHQKRKALKT	240
Db	181	DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSKGHQKRKALKT	240
Qy	241	TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI	300
Db	241	TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALGFFHCCLNPI	300
Qy	301	LYAFLGAKFKTSAQHALT SVSRGSSSLKILSKGKRGGHSSVSTESSESSFHSS	352
Db	301	LYAFLGAKFKTSAQHALT SVSRGSSSLKILSKGKRGGHSSVSTESSESSFHSS	352

RESULT 8

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ID O77488_CERAE PRELIMINARY; PRT; 352 AA.
AC O77488;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 30-MAY-2006, entry version 31.
DE CXCR4 receptor.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB015943; BAA31327.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000355; Chmkine_rcpt.
DR InterPro; IPR001277; CXCR4_rcpt.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00645; CXCCHEMOKINER4.

```

Query Match 98.7%; Score 1806; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 4.6e-131;
Matches 347; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

http://es/ScoreAccessWeb/GetItem.action?AppId=10785230&seqId=1105598&ItemName... 2/15/2007

DR PRINTS; PR00645; CXCCHMKINER4.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 352 AA; 39803 MW; 8018A4500FC887C0 CRC64;

Query Match 98.6%; Score 1805; DB 2; Length 352;
Best Local Similarity 98.3%; Pred. No. 5.5e-131;
Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEGISIIYTSIDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MEGISIIYTSIDNYTEEIGSGDYDSIKEPCFREENAHFNRIPLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFKAVHVIYTVNL 120
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
```

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SCORE 1.3 BuildDate: 11/17/2006

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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:15:46 ; Search time 26 Seconds
(without alignments)
1315.579 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIIYTSNDNYTEEMGSGD.....KRGGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%								Description
Result	Query	Match	Length	DB	ID					
No.	Score									
1	1830	100.0	352	2	A45747					neuropeptide Y/pep
2	1806	98.7	352	2	G00048					fusin (LESTRA) - c
3	1722.5	94.1	353	2	S28787					neuropeptide Y/pep
4	600.5	32.8	360	2	A57160					chemokine (C-C) re
5	582	31.8	367	2	JE0349					interferon-inducib
6	568	31.0	360	2	A53611					interleukin-8 rece
7	567	31.0	356	2	S42096					interleukin-8 rece
8	564.5	30.8	360	2	JC4587					chemokine (C-C) re
9	564	30.8	355	2	JQ1231					interleukin-8 rece
10	563	30.8	378	2	A55735					G protein-coupled
11	559.5	30.6	350	2	A39445					interleukin-8 rece
12	558	30.5	358	2	A53752					interleukin-8 rece
13	557	30.4	378	2	B55735					lymphocyte-specifi
14	549.5	30.0	355	2	JC4304					orphan G protein-c
15	544	29.7	327	2	S56162					MDCR15 protein - h
16	540	29.5	372	2	S26667					G protein-coupled
17	539	29.5	359	2	A48921					interleukin-8 rece
18	538	29.4	378	2	A45680					G protein-coupled
19	536	29.3	374	2	S42628					G protein-coupled

20	533.5	29.2	369	2	JC5068	G protein-coupled
21	529	28.9	374	2	S32785	G protein-coupled
22	528	28.9	374	2	I38450	chemokine (C-C) re
23	527	28.8	355	2	JC5067	G protein-coupled
24	519.5	28.4	383	2	S55594	G protein-coupled
25	514.5	28.1	354	2	I58186	probable G protein
26	512.5	28.0	360	2	JC2443	chemokine (C-C) re
27	509	27.8	355	2	G02436	chemokine (C-C) re
28	506	27.7	352	2	A43113	chemokine (C-C) re
29	503.5	27.5	355	2	A45177	chemokine (C-C) re
30	502.5	27.5	359	2	S15403	angiotensin II rec
31	501.5	27.4	350	2	JN0621	G protein-coupled
32	493.5	27.0	359	2	JC1104	angiotensin II rec
33	493.5	27.0	359	2	A42656	angiotensin II rec
34	488.5	26.7	359	2	S44425	angiotensin II rec
35	487.5	26.6	359	2	JQ1516	angiotensin II rec
36	485	26.5	362	2	JN0694	angiotensin II rec
37	484.5	26.5	359	2	A48857	angiotensin II rec
38	483.5	26.4	359	2	JH0621	angiotensin II rec
39	481	26.3	359	2	I49341	MIP-1 alpha recept
40	480.5	26.3	359	2	JC2134	angiotensin II rec
41	474.5	25.9	359	2	I39418	angiotensin II rec
42	473.5	25.9	362	2	A30341	G protein-coupled
43	472.5	25.8	359	2	JC1194	angiotensin II rec
44	469.5	25.7	355	2	I49339	macrophage inflamm
45	469.5	25.7	362	2	A39714	G protein-coupled

ALIGNMENTS

RESULT 1

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; receptor D2S201E

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: A45747; A53103; I53006; I59444; I69203; S32761

R;Federspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis, I.; Jirik, F.R. Genomics 16, 707-712, 1993

A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transm

A;Reference number: A45747; MUID:93315164; PMID:8325644

A;Accession: A45747

A;Molecule type: mRNA

A;Residues: 1-352 <FED>

A;Cross-references: UNIPROT:P61073; UNIPARC:UPI000000106C; GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g29

R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocy

A;Reference number: A53103; MUID:94103215; PMID:8276799

A;Accession: A53103

A;Molecule type: mRNA

A;Residues: 1-352 <LOE>

A;Cross-references: UNIPARC:UPI000000106C; EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100

R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A;Title: Molecular cloning, characterization, and localization of the human homolog to the reported bovine

A;Reference number: I53006; MUID:93319629; PMID:8329116

A;Accession: I53006

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <HER>

A;Cross-references: UNIPARC:UPI000000106C; GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928

R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Larhammar, D.; Wahlestedt Regul. Pept. 47, 247-258, 1993

A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neithe

A;Reference number: I59444; MUID:94052833; PMID:8234909

A;Accession: I59444

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <RE2>

A;Cross-references: UNIPARC:UPI000000106C; GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314

R;Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide rec

A;Reference number: I54751; MUID:94092629; PMID:7505609

A;Accession: I69203
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-352 <RES>
 A;Cross-references: UNIPARC:UPI000000106C; GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
 C;Genetics:
 A;Gene: GDB:NPY3R; NPY3
 A;Cross-references: GDB:230002; OMIM:162643
 A;Map position: 2q21-2q21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1830; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.2e-148;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
      |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
      |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
      |||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFY PN DLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
      |||
Db    181 DDRIYICDRFY PN DLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

Qy    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
      |||
Db    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
      |||
Db    301 LYAFLGAKFKTSAQH ALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352

```

RESULT 2

G00048

fusin (LESTRA) - crab-eating macaque

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C;Accession: G00048

R;Tatsumi, M.

submitted to GenBank, July 1996

A;Reference number: H00048

A;Accession: G00048

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <TAT>

A;Cross-references: UNIPROT:Q28474; UNIPARC:UPI0000127302; GB:D86579; NID:g1468948; PID:g1468949

C;Superfamily: vertebrate rhodopsin

Query Match 98.7%; Score 1806; DB 2; Length 352;
 Best Local Similarity 98.3%; Pred. No. 3.6e-146;
 Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
      |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
      |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
      |||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFASVSEA 180

Qy    181 DDRIYICDRFY PN DLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
      |||
Db    181 DDRIYICDRFY PN DLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

```



```

Db      206 FP-QVGRALRVQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFA 264
Qy      250 ACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFGLAKF 309
      || ||:: : :| : : : : | | : | : : |||||:||||:| ||
Db      265 VCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCCLNPLLYAFVGVKF 324
Qy      310 KTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSF 349
      :      | : |      :||      | : . ||:
Db      325 REQMMMLFTRLGRSD-----QRGPQRQPSSSRRESSW 356

```

RESULT 6

```

A53611
interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A a
A;Reference number: I37898; MUID:95014476; PMID:7929358
A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: UNIPROT:P25025; UNIPARC:UPI000004358A; EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: UNIPARC:UPI000000053D; EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.
A;Reference number: A53611; MUID:94209273; PMID:7512557
A;Accession: A53611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 6-360 <SPR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A;Reference number: A39446; MUID:91368200; PMID:1891716
A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including GRO, NAP-2,
C;Genetics:
A;Gene: GDB:IL8RB; IL8RA
A;Cross-references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

```

```

Query Match      31.0%; Score 568; DB 2; Length 360;
Best Local Similarity 35.3%; Pred. No. 8.7e-41;
Matches 132; Conservative 69; Mismatches 119; Indels 54; Gaps 11;

```

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Qy      9 SDNYT-----EEMGSGDYDSM-----KEPCFREANFNKIFLPTIYSIIFLTGIVGN 56
      ||::      ||: : ||      ||      ||: ||: ||::|| ||::||
Db      8 SDSFEDFWKGEDLSNYSYSTLPFFLLDAAPC-EPESLEINKYFVVIYALVFLSLLGN 66
Qy      57 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
      ||::|| : : ||::|| ||::||::||::||::|| || || || || || || : :
Db      67 SLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVVSLLK 126
Qy      117 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLTIPDFIF-- 174
      || || :|| ||:||||||| : : | | : : :| :|| :| :|
Db      127 EVNFYSGIILLACISVDYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 185
Qy      175 ----ANVSEADDRYICDRFPNDL--WVVVFQFHIMVGLILPGIVILSCYCIISKLSH 228
      :||| |      |      | : : :      | :| :|| || : |
Db      186 TVYSSNVSPA----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIIMLCYGTFLRTLFLK 240

```

```

Qy      229 SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITE 288
      :   || :||:   :|| | |||| : : | : : :||: || | : : : ||
Db      241 AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 300

Qy      289 ALAFFHCCLNPILYAFGLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTES---- 344
      |   | ||||:||||:| ||:   ||   ||||:   | :| :|
Db      301 ILGILHSCLNPLIYAFIGQKFR----HGL-----LKILAI-----HGLISKDSLPKD 343

Qy      345 -----ESSSFHSS 352
      ||| | :|
Db      344 SRPSFVGSSSGHTS 357

```

RESULT 7

S42096

interleukin-8 receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999

C;Accession: S42096

R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.

submitted to the EMBL Data Library, February 1994

A;Description: Molecular cloning of the rat IL8 receptor.

A;Reference number: S42096

A;Accession: S42096

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-356 <GOB>

A;Cross-references: UNIPARC:UPI00001778DE; EMBL:X77797

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 31.0%; Score 567; DB 2; Length 356;
 Best Local Similarity 36.3%; Pred. No. 1e-40;
 Matches 131; Conservative 68; Mismatches 126; Indels 36; Gaps 11;

```

Qy      10 DNYT-EEMSGDYDSMK-----EPCFREANANFNKIFLPTIYSIIFLTGI VGN 56
      ||:| :| ||| ||   ||   | : | : : || :| : |||
Db      7 DNFSLIEDFFSGDIDSYNFSSDPFPTLSDAAPC-PSANLDINRYAVVVIYVLVTLLSLVGN 65

Qy      57 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
      ||:| :| :| :| | :| :| ||| | :||| ||   | | ||:||||   :
Db      66 SLVMLVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQ 125

Qy      117 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFAN 176
      : | ||||:| | ||:||||||| |||: :| | | : :| :|:|:| ||
Db      126 EITFYSSVLLACISMDRYLAIVHATSTLIQKRHLV-KFVCITMWFSLVLSLPIFILRT 184

Qy      177 VSEAD-DRYICDRFYPN-----DLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSK 230
      :| :| :| | |   | || : | || :|| :|| ||   : | :
Db      185 TVKANPSTVVC---YENIGNNTSKWRVVLRLLPQTYGFLPLIMLCYGFETLRTLFKAH 241

Qy      231 GHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEAL 290
      || :||:   :|| | |||| | : | : : :||: || :| :|   :| |
Db      242 MGQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINK---ASEIL 298

Qy      291 AFFHCCLNPILYAFGLGAKFKTSAQHALTSVSRGSSLKILSK---GKRGHSSVSTESSESS 347
      | | ||||:||||:| ||:   || : : :|| | | | | :| :|
Db      299 GFLHSCLNPIIYAFIGQKFR----HGLLKIM--ANYGLVSKEFLAKEGRPSFVGSSSANT 352

Qy      348 S 348
      |
Db      353 S 353

```

RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.

Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human C

A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587

A;Molecule type: mRNA
 A;Residues: 1-360 <HOO>
 A;Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:
 A;Experimental source: thymus
 C;Genetics:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 30.8%; Score 564.5; DB 2; Length 360;
 Best Local Similarity 37.3%; Pred. No. 1.7e-40;
 Matches 109; Conservative 63; Mismatches 117; Indels 3; Gaps 2;

```
Qy      21 YDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMtdKYRLHL 80
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      22 YESMPKPCTKEGIKAFGEVFLPPLYSLVFLGLFGNSVVVLVLFKYKRLKSMtdVYLLNL 81

Qy      81 SVADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVH 140
      : : | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      82 AISDLLFVLSLPFWGYAAdQWVfGLGLCKIVSWMYLVGFYSGIFFIMLSIDRYLAIVH 141

Qy     141 ATNSQRPRKLLAEKVvYVGWIPALLLTIPDFIFANVSEADDRYICDRFYP--NDLWVVV 198
      | | : | | : : | | : : | : | : : | | : | : | : | : | : | :
Db     142 AVFSLKARTLTyGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQYSVNSTTWKVL 201

Qy     199 FQFQHIMVGLILPGIVILSCYCIiISKLSHSGHQKRKALKTTVILILAFFACWLPYYIG 258
      : : | | : | : | | : | | | | | : | : : : : : | | | : :
Db     202 SSLEINVLGLLIPLGIMLFWYSMIIRTlQHCKNEKNRAVRMIFGVVVLFLGEWTPYNV 261

Qy     259 ISIDSFILLEIiKQCEfENTVHKWISITEALAFFHCCCLNPILYAFLGAKFK 310
      : : : : | | : | | : | | | | | | | | : | | | | :
Db     262 LFLETLVELEVL-QDCTLERYLDYAIqATETLGFIHCCCLNPVIYFFLGEKFR 312
```

RESULT 9

JQ1231
 interleukin-8 receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: JQ1231; A46483
 R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, N.P.; Gerard, C.
 Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A;Title: Molecular characterization of the interleukin-8 receptor.
 A;Reference number: JQ1231; MUID:91378994; PMID:1898400
 A;Accession: JQ1231
 A;Molecule type: DNA
 A;Residues: 1-355 <BEC>
 A;Cross-references: UNIPROT:P21109; UNIPARC:UPI000012D4ED; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g16
 R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J. Immunol. 148, 1261-1264, 1992
 A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
 A;Reference number: A46483; MUID:92148149; PMID:1737938
 A;Accession: A46483
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-355 <LEE>
 A;Cross-references: UNIPARC:UPI000012D4ED; GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
 A;Experimental source: neutrophils
 A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIIP:81530)
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.8%; Score 564; DB 2; Length 355;
 Best Local Similarity 35.0%; Pred. No. 1.9e-40;
 Matches 123; Conservative 71; Mismatches 149; Indels 8; Gaps 6;

```
Qy      1 MEGISIYTSdNYTEEMGSdYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
      | : : | : | : | | | : | | : | : | : | : | : |
Db      8 MTDLTWfEDEFANATGMPPVEKDYSPCL-VVTQTLNkyVVVVIYALVFLLSLLGNsLVM 66

Qy     61 LVMGYQKKLRSMtdKYRLHLsvADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNL 120
      | | : | : | | | | | : | | | | | | | | | | | | | : | |
```

```

Db      67 LVILYSRNSRSDTVLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSILVKEVNF 126
Qy      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-SE 179
      || :||| ||:||||||| :  :: | | : :|| :|:|:| | | |
Db      127 YSGILLACISVDRLAIVHATRTLTKQRHLV-KFICLGIWALSILSLPFFLFRQVFSP 185
Qy      180 ADDRYIC--DRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQKRKA 237
      : :| | : : | : : | || :|| | | : | : | | :|
Db      186 NNSSPVCYEDLGHTAKWRMVLRLPHTFGFILPLLVMFLCYGFTLRTLQAHMGQKHRA 245
Qy      238 LKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCL 297
      :: :|| | |||| : : | : : :||: | : : : || | | | |
Db      246 MRVIFAVVLIFLLCWLPNLVLLADTLMRTHVIQETCQRNDIDRALDATEILGFLHSCL 305
Qy      298 NPILYAFLLGAKFKTSAQHALTSVSRG--SSLKILSKGKRGGHSSVSTESESS 347
      |||:|:| | | : | :|| | : | : : : :| || | :
Db      306 NPIIYAFIQNFRNGFLKML--AARGLISKEFLRHRVTSYTSSTNVPSN 354

```

RESULT 10

A55735

G protein-coupled receptor EB11 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C;Accession: A55735

R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W. Genomics 23, 643-650, 1994.

A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor encoded on human c

A;Reference number: A55735; MUID:95154835; PMID:7851893

A;Accession: A55735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: UNIPROT:P47774; UNIPARC:UPI00000274D1; GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g46

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

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Query Match      30.8%; Score 563; DB 2; Length 378;
Best Local Similarity 34.1%; Pred. No. 2.4e-40;
Matches 119; Conservative 77; Mismatches 147; Indels 6; Gaps 3;

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Db      29 TDDYIGENTTVDTYLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKR 88
Qy      69 LRSMTDKYRLHLSVADLLFVITLPEWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
      |::||| | |:|:|:|:| | ||| : | || :| | :| :| :|
Db      89 LKMTDTYLLNLAVADILFLILPFWAYSEAKSWIFGVYLCKGIFGIYKLSFFSGMLLLL 148
Qy      129 FISLDRLAIVHAT--NSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV--SEADRY 184
      ||:|:|:| | : | | | | | | | | | | | | | | : : |
Db      149 CISIDRYVAIVQAVSRHRHRARVLLISKLSVGIWMLALFLSIPELLYSGLQKNSGEDTL 208
Qy      185 ICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKTTVIL 244
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Db      209 RCSLSVSAQVEALITIQVQMVFGLVPLAMSFCYLIIIRTLQARNFERNKAIVIIAV 268
Qy      245 ILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAF 304
      :: | | ||| : : | | | | : : : | : | | | :| | | | |
Db      269 VVVFIVFQLPYNGVVLAAQTVANFNITNSSCETSKQLNIAYDVTYSLASVRCCVNPFLYAF 328
Qy      305 LGAKFKTSAQHALTSVSRGSS--LKILSKGKRGGHSSVSTESESSSFHS 351
      :| ||:: : | | : : : || | | : : |
Db      329 IGVKFRSDLFKLFDLGCLSQERLRHWSSCRHVRNASVSMEAETTTTFS 377

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RESULT 11

A39445

interleukin-8 receptor type A - human

N;Alternate names: interleukin-8 receptor, high-affinity

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C;Accession: I37449; I38710; I38711; A39445

R;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M. Genomics 16, 248-251, 1993

A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region of the human gen

A;Reference number: I37449; MUID:93252387; PMID:8486366
A;Accession: I37449
A;Molecule type: DNA
A;Residues: 1-350 <RES>
A;Cross-references: UNIPROT:P25024; UNIPARC:UPI0000050457; EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A a
A;Reference number: I37898; MUID:95014476; PMID:7929358
A;Accession: I38710
A;Molecule type: DNA
A;Residues: 1-350 <RE2>
A;Cross-references: UNIPARC:UPI0000050457; EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A;Accession: I38711
A;Molecule type: mRNA
A;Residues: 1-16 <RE3>
A;Cross-references: UNIPARC:UPI000000053C; EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R;Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A;Title: Structure and functional expression of a human interleukin-8 receptor.
A;Reference number: A39445; MUID:91368199; PMID:1840701
A;Accession: A39445
A;Molecule type: mRNA
A;Residues: 1-275,'T',277-350 <HOL>
A;Cross-references: UNIPARC:UPI0000043589; GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C;Genetics:
A;Gene: GDB:IL8RA
A;Cross-references: GDB:135039; OMIM:146929
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Qy	11	NYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLR	70
Db	16	NFT---GMPPADEDYSPCML-ETETLNKYVVIAYALVFLLSLLGNSLVMVLIVILYSRVGR	71
Qy	71	SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFI	130
Db	72	SVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACI	131
Qy	131	SLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLTLTPDFIFANVSEADDRY-ICDRF	189
Db	132	SVDRYLAIVHATRTLTQKRHLV-KFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEV	190
Qy	190	YPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKALKTTVILILA	247
Db	191	LGNDTAKWRMVLRLPHTFGFIVPLFVMLFCYGTFLRTLFKAHMGQKHRAMRVIFAVVLI	250
Qy	248	FFACWLPYYIGISIDSFILEI IKQGC EFENTVHKWISITEALAFFHCCLNPILYAF LGA	307
Db	251	FLLCWLPYNLVLLADTLMTQVIQESCERRNNIGRALDATEILGFLHSCCLNP I IYAFI GQ	310
Qy	308	KF-----K TSAQH ALTS	319
Db	311	NFRHGFLKILAMHGLVS	327

C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.5%; Score 558; DB 2; Length 358;
Best Local Similarity 35.4%; Pred. No. 6.1e-40;
Matches 128; Conservative 66; Mismatches 138; Indels 30; Gaps 8;

Qy	7	YTSDNYTEEMGSGDYDSM-----KEPCFREENANFNKIFLPTIYSIIFLTGIV	54
Db	4	FTWENYSYEDFFGDFSNYSYSTDLPPPTLLDSAPC-RSESLETNSYVVLITYILVFLLSL	62
Qy	55	GNGLVILVMGQYKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHV	114
Db	63	GNSLVMLVILYRSRSTCSVTDVYLLNLAIAIDLFPATTLPIWAASKVHGWTFTGPLCKVVSL	122
Qy	115	IYTVNLVYSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVYGVWIPALLTIPDFIF	174
Db	123	VKEVNFYSGILLLACISVDRYLAIVHATRTMIQKRHLV-KFICLSMWGVSLILSLPILF	181
Qy	175	AN-VSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGK	231
Db	182	RNAIFPNSSPVCYEDMGNSTAKWRMVLRLPQTFFGFIPLLVMLFCYVFTLRTLQFAHM	241
Qy	232	HQKRKALKTTVILILAFFACWLPPYYIGISIDSFILLEIKQGC EFENTVHKWISITEALA	291
Db	242	GQKHRAMRVIFAVVLIFLLCWLPYNLVLTDTLMRTHVIQETCERRNDIDRALDATEILG	301
Qy	292	FFHCCLNPILYAFLGAKF----KTSAQHALTSVSRGSSLKILSKGRGGHSSVSTES	346
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Db	354	TS 355	

RESULT 13

B55735

lymphocyte-specific G protein-coupled receptor EBI1 - human

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C;Species: Homo sapiens (man)

C>Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text change 09-Jul-2004

C;Accession: B55735; S52443

R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Genomics 23. 643-650. 1994

A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c

A;Reference number: A55735; MUID:95154835; PMID:7851893

A;Accession: B55735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: UNIPROT:P32248; UNIPARC:UPI0000001C2F; GB:L31581; NID:q468319; PIDN:AAA74231.1; PID:q46

R: Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.

submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transactivated by Epstein

A:Reference number: S52443

A:Accession: S52443

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 21-378 <BUR>

A:Cross-references: UNIPARC:UPI000014DEAD; EMBL:X84702

C: Genetics:

A:Gene: GDB:CMKBR7; EBI1; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C; Keywords: G protein-coupled receptor

Query Match 30.4%; Score 557; DB 2; Length 378;
Best Local Similarity 33.2%; Pred. No. 7.9e-40;
Matches 116; Conservative 79; Mismatches 148; Indels 6; Gaps 3;

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Db 29 TDDYIGDNTTVDYTLFESLCSKKDVRNEKAWFLPIMYSIICEVGLGNGLVVLTYIYFKR 88

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074033_us-10-785-230-1.rapbm.

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This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074033_us-10-785-230-1.rapbm.

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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:24:16 ; Search time 134 Seconds
(without alignments)
1215.298 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIIYTSIDNYTEEMGSGD.....KRGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	3	US-09-953-692-2	Sequence 2, Appli
2	1830	100.0	352	3	US-09-953-717-2	Sequence 2, Appli
3	1830	100.0	352	3	US-09-104-063-4	Sequence 4, Appli
4	1830	100.0	352	3	US-09-813-651B-85	Sequence 85, Appli
5	1830	100.0	352	4	US-10-151-274-4	Sequence 4, Appli
6	1830	100.0	352	4	US-10-225-567A-76	Sequence 76, Appli
7	1830	100.0	352	4	US-10-245-850-1	Sequence 1, Appli
8	1830	100.0	352	4	US-10-251-703-38	Sequence 38, Appli
9	1830	100.0	352	4	US-10-021-660-123	Sequence 123, App
10	1830	100.0	352	4	US-10-014-322A-126	Sequence 126, App

11	1830	100.0	352	4	US-10-239-423-79	Sequence 79, Appl
12	1830	100.0	352	4	US-10-170-385-331	Sequence 331, App
13	1830	100.0	352	4	US-10-160-401-3	Sequence 3, Appli
14	1830	100.0	352	4	US-10-341-434-178	Sequence 178, App
15	1830	100.0	352	4	US-10-372-683-2	Sequence 2, Appli
16	1830	100.0	352	4	US-10-440-464-78	Sequence 78, Appl
17	1830	100.0	352	4	US-10-452-015-1	Sequence 1, Appli
18	1830	100.0	352	4	US-10-211-462-81	Sequence 81, Appl
19	1830	100.0	352	4	US-10-666-689-4	Sequence 4, Appli
20	1830	100.0	352	4	US-10-181-906-10	Sequence 10, Appl
21	1830	100.0	352	4	US-10-706-265-10	Sequence 10, Appl
22	1830	100.0	352	4	US-10-785-230-1	Sequence 1, Appli
23	1830	100.0	352	5	US-10-486-471-20	Sequence 20, Appl
24	1830	100.0	352	5	US-10-985-324-2	Sequence 2, Appli
25	1830	100.0	352	6	US-11-021-951-189	Sequence 189, App
26	1830	100.0	352	6	US-11-028-922A-1	Sequence 1, Appli
27	1824	99.7	352	3	US-09-826-509-485	Sequence 485, App
28	1824	99.7	352	5	US-10-925-095-485	Sequence 485, App
29	1822	99.6	352	3	US-09-870-759-37	Sequence 37, Appl
30	1822	99.6	352	3	US-09-870-759-144	Sequence 144, App
31	1822	99.6	352	3	US-09-751-708A-37	Sequence 37, Appl
32	1822	99.6	352	3	US-09-751-708A-144	Sequence 144, App
33	1822	99.6	352	4	US-10-428-817A-33	Sequence 33, Appl
34	1822	99.6	352	4	US-10-428-817A-140	Sequence 140, App
35	1822	99.6	352	5	US-10-937-758A-37	Sequence 37, Appl
36	1822	99.6	352	5	US-10-937-758A-121	Sequence 121, App
37	1808	98.8	356	5	US-10-723-860-1280	Sequence 1280, Ap
38	1789	97.8	352	5	US-10-791-592-6	Sequence 6, Appli
39	1789	97.8	352	5	US-10-791-166-6	Sequence 6, Appli
40	1785	97.5	348	5	US-10-330-773-921	Sequence 921, App
41	1678.5	91.7	359	4	US-10-785-230-3	Sequence 3, Appli
42	1673	91.4	349	6	US-11-028-922A-2	Sequence 2, Appli
43	1633.5	89.3	355	5	US-10-330-773-918	Sequence 918, App
44	1042	56.9	209	4	US-10-292-798-688	Sequence 688, App
45	1037	56.7	209	4	US-10-017-161-790	Sequence 790, App

ALIGNMENTS

RESULT 1

US-09-953-692-2

; Sequence 2, Application US/09953692

; Patent No. US20020107195A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1{

; FILE REFERENCE: P50676C1

; CURRENT APPLICATION NUMBER: US/09/953,692

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 09/358,624

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Human

US-09-953-692-2

Query Match 100.0%; Score 1830; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-157;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-953-717-2

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; Sequence 2, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(
; FILE REFERENCE: P50676D1
; CURRENT APPLICATION NUMBER: US/09/953,717
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-953-717-2

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Query Match          100.0%; Score 1830; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-104-063-4

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; Sequence 4, Application US/09104063
; Patent No. US20020168356A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors

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; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,063
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-104-063-4

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Query Match          100.0%; Score 1830; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
         |||||||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQH ALT SVSRGSS LKILSKGKRGGHSSVSTESESSSFHSS 352
         |||||||
Db      301 LYAFLGAKFKTSAQH ALT SVSRGSS LKILSKGKRGGHSSVSTESESSSFHSS 352

```

```

RESULT 4
US-09-813-651B-85
; Sequence 85, Application US/09813651B

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```
; Publication No. US20030018438A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: Tan Hehir, Christina
; APPLICANT: Kates, Steven
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-007
; CURRENT APPLICATION NUMBER: US/09/813,651B
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-651B-85
```

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Query Match          100.0%; Score 1830; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 MEGISIIYSDNYTEEMGSGDYDSMKPECFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYSDNYTEEMGSGDYDSMKPECFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
        |||
Db    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 5

US-10-151-274-4

```
; Sequence 4, Application US/10151274
; Publication No. US20030064071A1
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-151-274-4

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
         |||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKQLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         |||||||
Db     61 LVMGYQKQLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180
         |||||||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180

Qy    181 DDYRICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
         |||||||
Db    181 DDYRICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
         |||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
         |||||||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 6

US-10-225-567A-76

; Sequence 76, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-76

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
         |||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKQLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         |||||||
Db     61 LVMGYQKQLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180
         |||||||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKV VYVGWIPALLLTIPDFIFANVSEA 180

Qy    181 DDYRICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
         |||||||
Db    181 DDYRICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
         |||||||
```

Db 241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

Db 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

RESULT 7

US-10-245-850-1

; Sequence 1, Application US/10245850

; Publication No. US20030124628A1

; GENERAL INFORMATION:

; APPLICANT: Burns, Jennifer M.

; APPLICANT: Miao, Zhenhua

; APPLICANT: Wei, Zheng

; APPLICANT: Howard, Maureen C.

; APPLICANT: Premack, Brett A.

; APPLICANT: Schall, Thomas J.

; APPLICANT: ChemoCentryx, Inc.

; TITLE OF INVENTION: Compositions and Methods for Detecting and Treating

; TITLE OF INVENTION: Diseases and Conditions Related to Chemokine Receptors

; FILE REFERENCE: 019934-003310US

; CURRENT APPLICATION NUMBER: US/10/245,850

; CURRENT FILING DATE: 2002-09-16

; PRIOR APPLICATION NUMBER: US 60/338,100

; PRIOR FILING DATE: 2001-11-30

; NUMBER OF SEQ ID NOS: 3.

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: CXCR4 chemokine receptor

US-10-245-850-1

Query Match 100.0%; Score 1830; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-157;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGISIIYTSNDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Db 1 MEGISIIYTSNDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy 61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Db 61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Db 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy 181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Db 181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy 241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Db 241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

Db 301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

RESULT 8

US-10-251-703-38

; Sequence 38, Application US/10251703

; Publication No. US20030148449A1

; GENERAL INFORMATION:

; APPLICANT: Kuliopulos, Athan

; APPLICANT: Covic, Lidiya

; TITLE OF INVENTION: G Protein Coupled Receptor Agonists and Antagonists and

; TITLE OF INVENTION: Methods of Activating and Inhibiting G Protein Coupled

; TITLE OF INVENTION: Receptors Using the Same

; FILE REFERENCE: NEMC-215 CIP

```

; CURRENT APPLICATION NUMBER: US/10/251,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 09/841,091
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/198,993
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Pepducin
; OTHER INFORMATION: Peptide Sequence
US-10-251-703-38

```

```

Query Match          100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEGISIYTSNDNYTEEMSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIYTSNDNYTEEMSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILEIISKQCEFENTVHKWISITEALAFFHCCLNPI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TVILILAFFACWLPYYIGISIDSFILEIISKQCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352

```

```

RESULT 9
US-10-021-660-123
; Sequence 123, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1e1 Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-123

```

```

Query Match          100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEGISIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||||||
Db      1 MEGISIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||||
Db      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGVWIPALLLTIPDFIFANVSEA 180
        |||||||
Db      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRIYCDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        |||||||
Db      181 DDRIYCDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||||||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||||||
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 10

US-10-014-322A-126

; Sequence 126, Application US/10014322A

; Publication No. US20030167129A1

; GENERAL INFORMATION:

; APPLICANT: Nestor, Jr., John

; APPLICANT: Wilson, Carol

; APPLICANT: Tan Hehir, Christina

; APPLICANT: Kates, Steven

; APPLICANT: Krstenansky, John

; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds

; FILE REFERENCE: CNS-008

; CURRENT APPLICATION NUMBER: US/10/014,322A

; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: US 60/243,587

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 09/813,651

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 09/813,653

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 09/813,448

; PRIOR FILING DATE: 2001-03-20

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 126

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-014-322A-126

Query Match 100.0%; Score 1830; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-157;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGISIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||||||
Db      1 MEGISIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||||
Db      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGVWIPALLLTIPDFIFANVSEA 180
        |||||||
Db      121 YSSVLILAFISLDRYLAI V HATNSQRPRKLLAEKV VYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRIYCDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        |||||||
Db      181 DDRIYCDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

```

```

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
          |||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
          |||
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 11

```

US-10-239-423-79
; Sequence 79, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-79

```

```

Query Match      100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEGISIIYTSNDYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
          |||
Db      1 MEGISIIYTSNDYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
          |||
Db      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLDRLYLAIIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
          |||
Db      121 YSSVLILAFISLDRLYLAIIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
          |||
Db      181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
          |||
Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
          |||
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 12

```

US-10-170-385-331
; Sequence 331, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan

```

```
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-331
```

```
Query Match          100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||||||
Db      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSMTDKYLRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db      61 LVMGYQKKLRSMTDKYLRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
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Db      121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
        |||||||
Db      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
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Db      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESSESSFHSS 352
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Db      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESSESSFHSS 352
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RESULT 13
US-10-160-401-3
; Sequence 3, Application US/10160401
; Publication No. US20030207281A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Koshy, Beena
; APPLICANT: Monroe, Glen
; APPLICANT: Rounds, Eileen
; TITLE OF INVENTION: HAPLOTYPES OF THE CXCR4 GENE
; FILE REFERENCE: MWH-0121US
; CURRENT APPLICATION NUMBER: US/10/160,401
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: PCT/US01/12268
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,025
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-160-401-3
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Query Match 100.0%; Score 1830; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.6e-157;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db    121 YSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 D DRYICDRFY PNDLWVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240
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Db    181 D DRYICDRFY PNDLWVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240

Qy    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Qy    301 LYAFLGAKFKTSAQH ALT SVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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US-10-341-434-178
 ; Sequence 178, Application US/10341434
 ; Publication No. US20030215835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OriGene Technologies
 ; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
 ; FILE REFERENCE: 9U 204 205 R1
 ; CURRENT APPLICATION NUMBER: US/10/341,434
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US 60/348,164
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: US 60/348,119
 ; PRIOR FILING DATE: 2002-01-15
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 178
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-341-434-178

Query Match 100.0%; Score 1830; DB 4; Length 352;
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Qy    181 D DRYICDRFY PNDLWVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240
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Db    181 D DRYICDRFY PNDLWVVFQFQHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKALKT 240

Qy    241 TVILILAFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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RESULT 15
US-10-372-683-2
; Sequence 2, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-2

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Db	61	LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL	120
Qy	121	YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA	180
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Qy	181	DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKALKT	240
Db	181	DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKALKT	240
Qy	241	TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI	300
Db	241	TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI	300
Qy	301	LYAFLGAKFKTSAQHALLTSVSRGSSLKILSKGKRGGHSSVSTESSESSFHSS	352
Db	301	LYAFLGAKFKTSAQHALLTSVSRGSSLKILSKGKRGGHSSVSTESSESSFHSS	352

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SCORE Search Results Details for Application 10785230 and Search Result 20070206_074037_us-10-785-230-1.rapbn.

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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:25:40 ; Search time 41 Seconds
(without alignments)
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Perfect score: 1830
Sequence: 1 MEGISIIYTSIDNYTEEMGSGD.....KRGHSSVSTESSESSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 571941 seqs, 137706945 residues

Total number of hits satisfying chosen parameters: 571941

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1830	100.0	352	6	US-10-505-928-745	Sequence 745, App
2	1830	100.0	352	6	US-10-511-937-2486	Sequence 2486, Ap
3	1830	100.0	352	6	US-10-511-937-2935	Sequence 2935, Ap
4	1830	100.0	352	6	US-10-511-937-3010	Sequence 3010, Ap
5	1830	100.0	352	6	US-10-219-051B-9078	Sequence 9078, Ap
6	1830	100.0	352	6	US-10-219-051B-9082	Sequence 9082, Ap
7	1830	100.0	352	7	US-11-371-354-68409	Sequence 68409, A
8	1827	99.8	363	6	US-10-545-557-19	Sequence 19, Appl

9	1824	99.7	352	7	US-11-404-939-485	Sequence 485, App
10	1785	97.5	348	6	US-10-540-898-921	Sequence 921, App
11	1678.5	91.7	359	7	US-11-437-734-2	Sequence 2, Appli
12	1673	91.4	349	6	US-10-219-051B-9076	Sequence 9076, Ap
13	1673	91.4	349	6	US-10-219-051B-9080	Sequence 9080, Ap
14	1671.5	91.3	352	7	US-11-437-734-8	Sequence 8, Appli
15	1633.5	89.3	355	6	US-10-540-898-918	Sequence 918, App
16	1100.5	60.1	230	7	US-11-437-734-4	Sequence 4, Appli
17	1042	56.9	209	7	US-11-214-063A-688	Sequence 688, App
18	850	46.4	188	7	US-11-437-734-6	Sequence 6, Appli
19	600.5	32.8	360	6	US-10-581-413-1	Sequence 1, Appli
20	581.5	31.8	359	6	US-10-219-051B-13793	Sequence 13793, A
21	576.5	31.5	368	6	US-10-511-937-2505	Sequence 2505, Ap
22	576.5	31.5	368	6	US-10-511-937-2931	Sequence 2931, Ap
23	576.5	31.5	368	7	US-11-302-678-59	Sequence 59, Appl
24	576.5	31.5	368	7	US-11-371-354-63307	Sequence 63307, A
25	569	31.1	367	7	US-11-392-789-2	Sequence 2, Appli
26	568	31.0	360	6	US-10-533-519-1184	Sequence 1184, Ap
27	568	31.0	360	6	US-10-219-051B-13795	Sequence 13795, A
28	568	31.0	360	7	US-11-242-111-19	Sequence 19, Appl
29	568	31.0	360	7	US-11-371-354-67277	Sequence 67277, A
30	563.5	30.8	350	7	US-11-371-354-61621	Sequence 61621, A
31	560.5	30.6	369	7	US-11-371-354-69405	Sequence 69405, A
32	560	30.6	374	6	US-10-669-920-3	Sequence 3, Appli
33	559.5	30.6	350	7	US-11-371-354-68399	Sequence 68399, A
34	559	30.5	361	6	US-10-669-920-374	Sequence 374, App
35	557.5	30.5	357	7	US-11-371-354-66939	Sequence 66939, A
36	557	30.4	378	6	US-10-511-937-2404	Sequence 2404, Ap
37	557	30.4	389	6	US-10-545-557-23	Sequence 23, Appl
38	557	30.4	475	7	US-11-520-715-56811	Sequence 56811, A
39	554.5	30.3	369	7	US-11-404-939-481	Sequence 481, App
40	553.5	30.2	364	6	US-10-669-920-377	Sequence 377, App
41	550	30.1	374	6	US-10-669-920-6	Sequence 6, Appli
42	549.5	30.0	355	6	US-10-516-032-8	Sequence 8, Appli
43	549.5	30.0	355	6	US-10-533-519-1109	Sequence 1109, Ap
44	549.5	30.0	355	7	US-11-371-354-56785	Sequence 56785, A
45	530	29.0	325	6	US-10-669-920-237	Sequence 237, App

ALIGNMENTS

RESULT 1

US-10-505-928-745

; Sequence 745, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 745

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-745

Query Match 100.0%; Score 1830; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.1e-164;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LVMGYQKKLR SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL	120
Db	61	LVMGYQKKLR SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL	120
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Db      241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
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RESULT 2

US-10-511-937-2486

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; Sequence 2486, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2486
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2486

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Query Match      100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-10-511-937-2935

; Sequence 2935, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2935

Query Match 100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
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Db 181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQRKALKT 240
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US-10-511-937-3010

; Sequence 3010, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3010
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-3010
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Query Match          100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREENANFNKIFLPTIYSIIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYSDNYTEEMSGSDYDSMKEPCFREENANFNKIFLPTIYSIIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
        |||
Db    181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 5

```
US-10-219-051B-9078
; Sequence 9078, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9078
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9078
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```
Query Match          100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
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Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

Qy      241 TVILILAFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLNPI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TVILILAFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQH ALT SVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LYAFLGAKFKTSAQH ALT SVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 6

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US-10-219-051B-9082
; Sequence 9082, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9082
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9082

```

```

Query Match      100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 YSSVLILAFISLD RYLAI V HATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 DDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240

Qy      241 TVILILAFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLNPI 300

```

```

Db      241  |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I 300
Qy      301  LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      301  LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 7

```

US-11-371-354-68409
; Sequence 68409, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68409
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-68409

```

```

Query Match      100.0%; Score 1830; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1  MEGISIIYSDNYTEEMGSGDYDSMKPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      1  MEGISIIYSDNYTEEMGSGDYDSMKPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy      61  LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      61  LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy      121 YSSVLILAFISLDRLYLAI VHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 180
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      121 YSSVLILAFISLDRLYLAI VHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 180

Qy      181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      181 DDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKT 240

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      241 TVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLNPI 300

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||||T|||L|||A|||F|||A|||C|||W|||P|||Y|||I|||G|||I|||S|||D|||S|||F|||I|||L|||E|||I|||K|||Q|||G|||C|||E|||F|||E|||N|||T|||V|||H|||K|||W|||I|||S|||I|||T|||E|||A|||L|||A|||F|||H|||C|||C|||L|||N|||P|||I
Db      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

```

RESULT 8

```

US-10-545-557-19
; Sequence 19, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:

```



```
; APPLICANT: ANOSYS
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING ANTIBODY
; TITLE OF INVENTION: REPERTOIRES
; FILE REFERENCE: 3665-158
; CURRENT APPLICATION NUMBER: US/10/545,557
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: PCT/IB2004/000888
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US60/447,291
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 363
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CXCR4 + HA Tag
US-10-545-557-19
```

```
Query Match          99.8%; Score 1827; DB 6; Length 363;
Best Local Similarity 99.7%; Pred. No. 6.1e-164;
Matches 351; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEGISIIYTSNDNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 60
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 LEGISIIYTSNDNYTEEMGSGDYDSMKPEPCFREENANFNKIFLPTIYSIIFLTGVGNGLVI 71

Qy      61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 131

Qy      121 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 180
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      132 YSSVLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEA 191

Qy      181 DDRIYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 240
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      192 DDRIYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKALKT 251

Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      252 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 311

Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSSVTESESSSFHSS 352
         :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      312 LYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSSVTESESSSFHSS 363
```

RESULT 9

```
US-11-404-939-485
; Sequence 485, Application US/11404939
; Publication No. US20060183164A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/11/404,939
; CURRENT FILING DATE: 2006-04-14
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-404-939-485
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Query Match 99.7%; Score 1824; DB 7; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1.1e-163;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 180

Qy    181 D DRYICDRFY PN DLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
        |||
Db    181 D DRYICDRFY PN DLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy    301 LYAFLGAKFKTSAQH ALT SVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||
Db    301 LYAFLGAKFKTSAQH ALT SVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

```

RESULT 10

US-10-540-898-921
 ; Sequence 921, Application US/10540898
 ; Publication No. US20060166213A1
 ; GENERAL INFORMATION:
 ; APPLICANT: David W. Morris
 ; APPLICANT: Marc Malandro
 ; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
 ; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
 ; CURRENT APPLICATION NUMBER: US/10/540,898
 ; CURRENT FILING DATE: 2005-06-27
 ; PRIOR APPLICATION NUMBER: US 10/330,773
 ; PRIOR FILING DATE: 2002-12-27
 ; NUMBER OF SEQ ID NOS: 981
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 921
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-540-898-921

Query Match 97.5%; Score 1785; DB 6; Length 348;
 Best Local Similarity 98.6%; Pred. No. 5.3e-160;
 Matches 347; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

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Qy      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
        |||
Db      1 MEGISIIYTS DNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
        |||
Db     61 LVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVN- 119

Qy    121 YSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 180
        |||
Db    120 -KSVLILAFISLD RYLAIVHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANVSEA 178

Qy    181 D DRYICDRFY PN DLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 240
        |||
Db    179 D DRYICDRFY PN DLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKT 238

Qy    241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
        |||
Db    239 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITE--AFFHCCLNPI 296

Qy    301 LYAFLGAKFKTSAQH ALT SVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
        |||

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http://es/ScoreAccessWeb/GetItem.action?AppId=10785230&seqId=1105606&ItemName... 2/15/2007

```
; SOFTWARE: Perl script
; SEQ ID NO 9076
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
; DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9076
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```
Query Match          91.4%; Score 1673; DB 6; Length 349;
Best Local Similarity 90.8%; Pred. No. 1.9e-149;
Matches 317; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
```

```
Qy      4 ISITYSDNYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
        : |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      1 MEITYSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy      64 GYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNLYSS 123
        |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      61 GYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKfLCKAVHIIYTVNLYSS 120

Qy      124 VLILAFISLDryLAIVHATNSQRPRKLLAEKVVYVGWIPALLLTIPDFIFANVSEADDR 183
        |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      121 VLILAFISLDryLAIVHATNSQSARKLLAEKAVYVGWIPALLLTIPDIIFADVsqGDGR 180

Qy      184 YICDRFYpNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKALKTTVI 243
        ||||| ||: ||:||||| ||||:| ||:||||| |||||:|||||
Db      181 YICDRLYpDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKALKTTVI 240

Qy      244 LILAFACWLPYYIGISIDSfILLEIKQGEFENTVHKWISITEALAFFHCCLNPILYA 303
        |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      241 LILAFACWLPYYVGISIDSfILLEVIKQGEFESVVKWISITEALAFFHCCLNPILYA 300

Qy      304 FLGAKFKtSAQHAlTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
        |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      301 FLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

RESULT 13

```
US-10-219-051B-9080
; Sequence 9080, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9080
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
; DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9080
```

```
Query Match          91.4%; Score 1673; DB 6; Length 349;
Best Local Similarity 90.8%; Pred. No. 1.9e-149;
Matches 317; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
```

```
Qy      4 ISITYSDNYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
        : |||||:|:||||| ||||:| ||:||||| |||||:|||||
Db      1 MEITYSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy      64 GYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNLYSS 123
```

```

Db      61 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120
Qy      124 VLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANVSEADDR 183
Db      121 VLILAFISLDRLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV SQGDGR 180
Qy      184 YICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSGHQKRKALKTTVI 243
Db      181 YICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSGHQKRKALKTTVI 240
Qy      244 LILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 303
Db      241 LILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVKWISITEALAFFHCCLNPILYA 300
Qy      304 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
Db      301 FLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349

```

RESULT 14

```

US-11-437-734-8
; Sequence 8, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadimitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: IIZASA, Hisashi
; APPLICANT: YOSHIDA, Nobuaki
; APPLICANT: NAKAJIMA, Toshihiro
; APPLICANT: YOSHIE, Osamu
; TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
; FILE REFERENCE: 1422-386P
; CURRENT APPLICATION NUMBER: US/11/437,734
; CURRENT FILING DATE: 2006-05-22
; PRIOR APPLICATION NUMBER: US/09/367,052
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-437-734-8

```

```

Query Match          91.3%; Score 1671.5; DB 7; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.6e-149;
Matches 318; Conservative 18; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 IYTSNDNYTEEMSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 65
Db      1 IYTSNDNYSEEVGSDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 60
Qy      66 QKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125
Db      61 QKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 120
Qy      126 ILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----SEA 180
Db      121 ILAFISLDRLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDISQG 180
Qy      181 DRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSGHQKRKALKT 240
Db      181 DRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLHSHSGHQKRKALKT 240
Qy      241 TVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
Db      241 TVILILAFFACWLPYYVGISIDSFILLGVKQGCD FESIVHKWISITEALAFFHCCLNPI 300
Qy      301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
Db      301 LYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

```

RESULT 15

US-10-540-898-918
; Sequence 918, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-540-898-918

Query Match 89.3%; Score 1633.5; DB 6; Length 355;
Best Local Similarity 88.7%; Pred. No. 1e-145;
Matches 314; Conservative 19; Mismatches 12; Indels 9; Gaps 3;

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Qy      4 ISITYSDNYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
       :|||||||:|:||||||| |||||:| :|:||||||| |||||:|||||||
Db      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65

Qy     64 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db     66 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVN--KS 123

Qy    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 183

Qy    179 EADDRIYCDRFPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238
       : ||||||| ||: ||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    184 QGDDRIYCDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 243

Qy    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    244 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITE--AFFHCCLN 301

Qy    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    302 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 355
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Search completed: February 6, 2007, 14:31:22
Job time : 42.5963 secs

start

SCORE 1.3 BuildDate: 11/17/2006

6	1758.5	94.2	349	10	AEF38900	Aef38900 Rat chemo
7	1758.5	94.2	349	10	AEK47825	Aek47825 Rat chemo
8	1744.5	93.4	349	7	ADE63141	Ade63141 Rat Prote
9	1744.5	93.4	349	7	ADE63145	Ade63145 Rat Prote
10	1744.5	93.4	349	10	AEE66169	Aee66169 Rat CXCR4
11	1678.5	89.9	352	2	AAR68812	Aar68812 Human mon
12	1678.5	89.9	352	2	AAR80757	Aar80757 Chemokine
13	1678.5	89.9	352	2	AAY39993	Aay39993 Human CXC
14	1678.5	89.9	352	3	AAY52507	Aay52507 Human CXC
15	1678.5	89.9	352	4	AAE06690	Aae06690 Human neu
16	1678.5	89.9	352	4	AAG79088	Aag79088 Amino aci
17	1678.5	89.9	352	4	AAG80123	Aag80123 Human CXC
18	1678.5	89.9	352	5	AAO14003	Aao14003 Human cys
19	1678.5	89.9	352	5	ABP52651	Abp52651 Human CXC
20	1678.5	89.9	352	5	ABG32977	Abg32977 Human CXC
21	1678.5	89.9	352	5	ABG33065	Abg33065 Human CXC
22	1678.5	89.9	352	5	ABP65183	Abp65183 Hypoxia-r
23	1678.5	89.9	352	5	AAG78471	Aag78471 CXCR4 pro
24	1678.5	89.9	352	6	ABP96794	Abp96794 Human COP
25	1678.5	89.9	352	6	ABU03495	Abu03495 Angiogene
26	1678.5	89.9	352	6	ABR58581	Abr58581 Human can
27	1678.5	89.9	352	6	ABP97733	Abp97733 Amino aci
28	1678.5	89.9	352	6	ABP81796	Abp81796 Human CXC
29	1678.5	89.9	352	7	ADC98646	Adc98646 Human CXC
30	1678.5	89.9	352	7	ADE63147	Ade63147 Human Pro
31	1678.5	89.9	352	7	ADE63143	Ade63143 Human Pro
32	1678.5	89.9	352	7	ADF90878	Adf90878 Human hep
33	1678.5	89.9	352	7	ADO16837	Ado16837 CXCR4 ami
34	1678.5	89.9	352	7	ADN95821	Adn95821 Human BEC
35	1678.5	89.9	352	8	ADH17079	Adh17079 Human orp
36	1678.5	89.9	352	8	ADN04756	Adn04756 Antipsori
37	1678.5	89.9	352	8	ADO29271	Ado29271 Human GPC
38	1678.5	89.9	352	8	ADP12477	Adp12477 Protein e
39	1678.5	89.9	352	8	ADP12926	Adp12926 Protein e
40	1678.5	89.9	352	8	ADP13001	Adp13001 Protein e
41	1678.5	89.9	352	8	ADO19692	Ado19692 Human PRO
42	1678.5	89.9	352	8	ADO19832	Ado19832 Human PRO
43	1678.5	89.9	352	8	ADO20013	Ado20013 Human PRO
44	1678.5	89.9	352	8	ADP44055	Adp44055 Human CXC
45	1678.5	89.9	352	8	ADQ14488	Adq14488 Human che

ALIGNMENTS

RESULT 1

AAW64778

ID AAW64778 standard; protein; 359 AA.

XX

AC AAW64778;

XX

DT 20-NOV-1998 (first entry)

XX

DE A murine CXC chemokine receptor.

XX

KW Mouse; CXC chemokine receptor; pre-B cell line DW34;

KW CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1; HIV infection;

KW screening; inhibitor; AIDS.

XX

OS Mus sp.

XX

PN WO9835035-A1.

XX

PD 13-AUG-1998.

XX

PF 07-FEB-1997; 97WO-JP000299.

XX

PR 07-FEB-1997; 97WO-JP000299.

XX

PA (SHIO) SHIONOGI & CO LTD.

XX

PI Kishimoto T, Nagasawa T, Tachibana K, Iizasa H, Yoshida N;

PI Nakajima T, Yoshie O;

XX

DR WPI; 1998-447232/38.

DR N-PSDB; AAV46370.

XX
PT Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell stimulatory
PT factor - is useful for screening of potential HIV infection and AIDS
PT inhibitors.
XX
PS Claim 1; Page 54-56; 76pp; Japanese.
XX
CC The present sequence represents a murine CXC chemokine receptor which
CC binds to the mouse CXC chemokine pre-B cell stimulatory factor PBSF/SDF-
CC 1. The nucleic acid is isolated from mouse pre-B cell line DW34. The
CC receptor and cells expressing it can be used in the study and mapping of
CC the mechanism of HIV infection and in screening of potential inhibitors
CC of HIV infection and the development of AIDS
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-214;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEPISVSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
        |||
Db      1 MEPISVSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy     61 VILVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
        |||
Db     61 VILVMGYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy    121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 180
        |||
Db    121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 180

Qy    181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240
        |||
Db    181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240

Qy    241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
        |||
Db    241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy    301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSSVSTESSESSFHSS 359
        |||
Db    301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSSVSTESSESSFHSS 359

```

RESULT 2

AAY39994

ID AAY39994 standard; protein; 359 AA.

XX

AC AAY39994;

XX

DT 16-DEC-1999 (first entry)

XX

DE Mouse CXCR4 protein sequence.

XX

KW CXCR4; mouse; neovascularisation; inhibitor; solid cancer; therapy;

KW tissue repairing agent; vascularisation.

XX

OS Mus sp.

XX

PN W09948528-A1.

XX

PD 30-SEP-1999.

XX

PF 23-MAR-1999; 99WO-JP001448.

XX

PR 24-MAR-1998; 98JP-00095448.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

PA (KISH/) KISHIMOTO T.

XX

PI Kishimoto T, Nagasawa T, Tachibana K;

XX

DR WPI; 1999-591042/50.

DR N-PSDB; AA227611.

XX

PT CXCR4-potentiating agents and methods useful for inhibiting
PT neovascularization, and treating solid cancers.
XX
PS Disclosure; Page 49-50; 63pp; Japanese.
XX
CC This sequence is the mouse CXCR4 protein. The invention relates to
CC remedies inhibiting neovascularisation, remedies for solid cancer,
CC remedies for diseases pathologically caused by neovascularisation and
CC tissue repairing agents containing as the active ingredient a substance
CC capable of potentiating CXCR4. Based on a finding that vascularisation is
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
CC remedies inhibiting vascularisation which contain as the active
CC ingredient a substance capable of potentiating CXCR4, remedies for solid
CC cancer, remedies for diseases pathologically caused by neovascularisation
CC and tissue repairing agents containing as the active ingredient a
CC substance capable of potentiating CXCR4. It is also possible to establish
CC methods for treatment with the use of these remedies .
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-214;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
      |||
Db      1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60

Qy     61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
      |||
Db     61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy    121 NLYSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIFADVS 180
      |||
Db    121 NLYSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIFADVS 180

Qy    181 QGDISQGD DRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQ 240
      |||
Db    181 QGDISQGD DRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQ 240

Qy    241 KRKALKTTVILILAFFACWLPYYVGISIDS FILLGVIKQGCD FESIVHKWISITEALAFF 300
      |||
Db    241 KRKALKTTVILILAFFACWLPYYVGISIDS FILLGVIKQGCD FESIVHKWISITEALAFF 300

Qy    301 HCCLNPILYAFLGAKFKSSAQHALNMSR GSSLKILSKGKRGHSSVSTESESSSFHSS 359
      |||
Db    301 HCCLNPILYAFLGAKFKSSAQHALNMSR GSSLKILSKGKRGHSSVSTESESSSFHSS 359

```

RESULT 3

ADO29272

ID ADO29272 standard; protein; 359 AA.

XX

AC ADO29272;

XX

DT 29-JUL-2004 (first entry)

XX

DE Mouse GPCR CXCR4, SEQ ID NO:373.

XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; receptor.

XX

OS Mus musculus.

XX
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 XX
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX
 DR WPI; 2004-390329/36.
 DR N-PSDB; ADO30145.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 373; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 8; Length 359;
 Best Local Similarity 100.0%; Pred. No. 2.1e-214;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
 Db 1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60

Qy 61 VILVMGYQKKLRSM TD KYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
 Db 61 VILVMGYQKKLRSM TD KYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy 121 NLYSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIFADV S 180
 Db 121 NLYSSVLILAFISLDRYLAI VHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIFADV S 180

Qy 181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCI IISKLSHSGKHQ 240

```

Db      181  QGDISQGD DRYICDR LYPDSLW MVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQ 240
Qy      241  KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFF 300
Db      241  KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFF 300
Qy      301  HCCLNPILYAF LGA FKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
Db      301  HCCLNPILYAF LGA FKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359

```

RESULT 4

ADQ97941

ID ADQ97941 standard; protein; 359 AA.

XX

AC ADQ97941;

XX

DT 07-OCT-2004 (first entry)

XX

DE Mouse cancer associated sequence MP11-026, SEQ ID 918.

XX

KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse.

XX

OS Mus musculus.

XX

PN WO2004060304-A2.

XX

PD 22-JUL-2004.

XX

PF 22-DEC-2003; 2003WO-US041389.

XX

PR 27-DEC-2002; 2002US-00330773.

XX

PA (SAGR-) SAGRES DISCOVERY INC.

XX

PI Morris DW, Malandro MS;

XX

DR WPI; 2004-543781/52.

XX

PT New isolated cancer associated nucleic acids comprising at least 10
 PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
 PT cancers such as leukemia and lymphoma.

XX

PS Claim 1; SEQ ID NO 918; 199pp; English.

XX

CC The present invention relates to cancer associated sequences (ADQ97025-
 CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
 CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic formate directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 2.1e-214;

Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
Db      1  MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
Qy      61  VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
Db      61  VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
Qy      121 NLYSSVLILAFISLD RYLAI VHATNSQRPRKLLAEKAVYVGWIPALLTIPDFIFADV S 180
Db      121 NLYSSVLILAFISLD RYLAI VHATNSQRPRKLLAEKAVYVGWIPALLTIPDFIFADV S 180
Qy      181 QGDISQGD DRYICDR LYPDSLW MVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQ 240
Db      181 QGDISQGD DRYICDR LYPDSLW MVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQ 240
Qy      241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFF 300

```

```

Db      241 |||||
          KKKALKTTTILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
Qy      301 HCCLNPILYAFLGAKFKSSAQHALNMSRGSLLKILSKGKRGGHSSVSTESESSSFHSS 359
          |||||
Db      301 HCCLNPILYAFLGAKFKSSAQHALNMSRGSLLKILSKGKRGGHSSVSTESESSSFHSS 359

```

RESULT 5
AEF38898

```

ID  AEF38898 standard; protein; 357 AA.
XX
AC  AEF38898;
XX
DT  23-MAR-2006 (first entry)
XX
DE  Mouse chemokine (C-X-C motif) receptor 4.
XX
KW  non-insulin dependent diabetes; antidiabetic; obesity; anorectic;
KW  insulin resistance; diagnosis.
XX
OS  Mus musculus.
XX
PN  WO2006007400-A2.
XX
PD  19-JAN-2006.
XX
PF  15-JUN-2005; 2005WO-US021297.
XX
PR  16-JUN-2004; 2004US-0580448P.
XX
PA  (META-) METABOLEX INC.
XX
PI  Moodie SA, Zhang F, Rack PG, Shang J, Lavan BE, Allan B, Wong C;
PI  Gregoire F, Perez G, Waters S;
XX
DR  WPI; 2006-110285/11.
DR  N-PSDB; AEF38897.
XX
PT  Identifying an agent for treating an obese, diabetic or pre-diabetic
PT  individual comprises selecting an agent that modulates the expression or
PT  activity of the polypeptide or that binds to the polypeptide.
XX
PS  Claim 9; SEQ ID NO 72; 281pp; English.
XX
CC  The invention relates to identifying an agent for treating an obese,
CC  diabetic or pre-diabetic individual comprises selecting an agent that
CC  modulates the expression or activity of the polypeptide or that binds to
CC  the polypeptide. The method comprises contacting an agent to a
CC  polypeptide encoded by a polynucleotide that hybridizes to a nucleic acid
CC  encoding any one the proteins included in the sequence listing (in 50%
CC  formamide, 5 x SSC, and 1% SDS at 42 degrees C followed by a wash in 0.2
CC  x SSC, and 0.1% SDS at 55 degrees C) and selecting an agent that
CC  modulates the expression or activity of the polypeptide, or that binds to
CC  the polypeptide, thus identifying an agent for treating an obese,
CC  diabetic or pre-diabetic individual. The method further comprises
CC  detecting whether the selected agent modulates weight and/or obesity, or
CC  insulin sensitivity. The polypeptide is expressed in a cell and the cell
CC  is contacted with the agent. The method is useful for identifying an
CC  agent for treating obesity or diabetes. The present sequence represents a
CC  full length mouse polypeptide of the invention.
XX
SQ  Sequence 357 AA;

```

```

Query Match      99.0%; Score 1848; DB 10; Length 357;
Best Local Similarity 99.4%; Pred. No. 3.9e-212;
Matches 357; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```

```

Qy      1 MEPISVSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
          |||||
Db      1 MEPI--SIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 58
Qy      61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFVAVDAMADWYFGKFLCKAVHIIYTV 120
          |||||
Db      59 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFVAVDAMADWYFGKFLCKAVHIIYTV 118

```

```

Qy      121 NLYSSVLILAFISLDRLYLAIIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 180
          |||
Db      119 NLYSSVLILAFISLDRLYLAIIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 178

Qy      181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQ 240
          |||
Db      179 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQ 238

Qy      241 KRKALKTTVILILAFFACWLPPYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
          |||
Db      239 KRKALKTTVILILAFFACWLPPYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 298

Qy      301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
          |||
Db      299 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGHSSVSTESESSSFHSS 357

```

RESULT 6

AEF38900

ID AEF38900 standard; protein; 349 AA.

XX

AC AEF38900;

XX

DT 23-MAR-2006 (first entry)

XX

DE Rat chemokine (C-X-C motif) receptor 4.

XX

KW non-insulin dependent diabetes; antidiabetic; obesity; anorectic;
KW insulin resistance; diagnosis.

XX

OS Rattus norvegicus.

XX

PN WO2006007400-A2.

XX

PD 19-JAN-2006.

XX

PF 15-JUN-2005; 2005WO-US021297.

XX

PR 16-JUN-2004; 2004US-0580448P.

XX

PA (META-) METABOLEX INC.

XX

PI Moodie SA, Zhang F, Rack PG, Shang J, Lavan BE, Allan B, Wong C;
PI Gregoire F, Perez G, Waters S;

XX

DR WPI; 2006-110285/11.

DR N-PSDB; AEF38899.

XX

PT Identifying an agent for treating an obese, diabetic or pre-diabetic
PT individual comprises selecting an agent that modulates the expression or
PT activity of the polypeptide or that binds to the polypeptide.

XX

PS Claim 9; SEQ ID NO 74; 281pp; English.

XX

CC The invention relates to identifying an agent for treating an obese,
CC diabetic or pre-diabetic individual comprises selecting an agent that
CC modulates the expression or activity of the polypeptide or that binds to
CC the polypeptide. The method comprises contacting an agent to a
CC polypeptide encoded by a polynucleotide that hybridizes to a nucleic acid
CC encoding any one the proteins included in the sequence listing (in 50%
CC formamide, 5 x SSC, and 1% SDS at 42 degrees C followed by a wash in 0.2
CC x SSC, and 0.1% SDS at 55 degrees C) and selecting an agent that
CC modulates the expression or activity of the polypeptide, or that binds to
CC the polypeptide, thus identifying an agent for treating an obese,
CC diabetic or pre-diabetic individual. The method further comprises
CC detecting whether the selected agent modulates weight and/or obesity, or
CC insulin sensitivity. The polypeptide is expressed in a cell and the cell
CC is contacted with the agent. The method is useful for identifying an
CC agent for treating obesity or diabetes. The present sequence represents a
CC full length rat polypeptide of the invention.

XX

SQ Sequence 349 AA;

Query Match 94.2%; Score 1758.5; DB 10; Length 349;
Best Local Similarity 96.0%; Pred. No. 2.1e-201;
Matches 340; Conservative 4; Mismatches 5; Indels 5; Gaps 1;

Qy	65	VSIYTS	SDNYSEE	VSGSDY	DSNKEP	CFRDENV	HFNRI	FLPTIY	FIIFLT	GIVGN	GLVIL	VM	65
Db	60	MEIYTS	SDNYSEE	VSGSDY	DSNKEP	CFRDENV	FNRI	FLPTIY	FIIFLT <td>GIVGN</td> <td>GLVIL</td> <td>VM</td> <td>60</td>	GIVGN	GLVIL	VM	60
Qy	125	GYQKK	LRSM	TDKYR	LHLSV	ADLLF	VITL	PFWAV	DAMAD	WYFGK	FLCKA	VHIIY	TVNL
Db	120	GYQKK	LRSM	TDKYR	LHLSV	ADLLF	VITL	PFWAV	DAMAD	WYFGK	FLCKA	VHIIY	TVNL
Qy	185	VLILAF	ISLD	RYLA	IVHAT	NSQR	PRKLL	AEKAV	YVGV	WIPALL	TIPDF	IFADV	SQGD
Db	175	VLILAF	ISLD	RYLA	IVHAT	NSQR	PRKLL	AEKAV	YVGV	WIPALL	TIPDI	IFADV	-----S
Qy	245	QGDD	RYIC	DRLYP	DSLWM	VVFQ	FQHIM	VGLIL	PGIV	ILSCY	CIIS	KL	SHSK
Db	235	QGDG	RYIC	DRLYP	DSLWM	VVFQ	FQHIM	VGLIL	PGIV	ILSCY	CIIS	KL	SHSK
Qy	305	KTTV	ILILA	FFAC	WL	PYYV	GISID	SFILL	GVIKQ	GCD	FE	SIVH	KWIS
Db	295	KTTV	ILILA	FFAC	WL	PYYV	GISID	SFILLE	VIKQ	GCE	FE	SIVH	KWIS
Qy	359	PILYA	FLGA	KFKSS	AAH	ALNS	MSRGS	SSLK	ILSK	GKRG	HSSV	STES	ESSS
Db	349	PILYA	FLGA	KFKSS	AAH	ALNS	MSRGS	SLK	ILSK	GKRG	HSSV	STES	ESSS

CC phospholipidosis disease in a mammal (comprising detecting expression
 CC fluctuation of one or more genes, being correlated to the onset of the
 CC phospholipidosis disease, in a sample collected from a mammal, where at
 CC least one gene has a base sequence that is the same or substantially same
 CC as a nucleic acid given in the specification). The nucleic acid sequences
 CC are useful for determining phospholipidosis disease in a mammal (such as
 CC human, rat, mouse, dog or monkey), using a sample such as blood or
 CC lymphocyte, where the phospholipidosis disease originates from a compound
 CC or the mammal had administered or exposed to the compound, and the
 CC compound has cationic amphiphilic drug structure. The reagent enables
 CC rapid, simple and precise or non-invasive determination of
 CC phospholipidosis disease in a mammal, with decreased appearance frequency
 CC of false-positive results. The present sequence represents a protein
 CC encoded by a rat cDNA a change in expression of which correlates with
 CC onset of phospholipidosis.

XX

SQ Sequence 349 AA;

Query Match 94.2%; Score 1758.5; DB 10; Length 349;
 Best Local Similarity 96.0%; Pred. No. 2.1e-201;
 Matches 340; Conservative 4; Mismatches 5; Indels 5; Gaps 1;

QY 6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
 : ||||||||||||||||||||||||||||| :|||||||||||||||||||||||||||
 Db 1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

QY 66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
 ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
 Db 61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

QY 126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
 ||||||||||||||||||||||||||||| ||||||| ||||| |
 Db 121 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDIIFADV-----S 175

QY 186 QGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
 ||| ||||||||||||||||||||||||| |||||||||||||||||||||||||
 Db 176 QGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 235

QY 246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
 ||||||||||||||||||||||||| |||||:||||:|||||||||||||||
 Db 236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCFESVVKWISITEALAFFHCCLN 295

QY 306 PILYAFGLAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
 ||||||||||||||||||||||||| |||||||||||||||||||||||||
 Db 296 PILYAFGLAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 349

RESULT 8

ADE63141

ID ADE63141 standard; protein; 349 AA.

XX

AC ADE63141;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein 008565, SEQ ID NO 9076.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX
DR WPI; 2003-268312/26.
DR GENBANK; 008565.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 349 AA;

Query Match 93.4%; Score 1744.5; DB 7; Length 349;
Best Local Similarity 95.5%; Pred. No. 9.9e-200;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

Qy 6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
: ||||| :
Db 1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60
Qy 66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
: ||||| :
Db 61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120
Qy 126 VLILAFISLDRLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVVSQGDIS 185
: ||||| :
Db 121 VLILAFISLDRLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV----S 175
Qy 186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGHQRKAL 245
: ||||| :
Db 176 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGHQRKAL 235
Qy 246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
: ||||| :
Db 236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQCFESVVKWISITEALAFFHCCLN 295
Qy 306 PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 359
: ||||| :
Db 296 PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 349

RESULT 9
ADE63145
ID ADE63145 standard; protein; 349 AA.
XX
AC ADE63145;
XX
DT 29-JAN-2004 (first entry)
XX

DE Rat Protein 008565, SEQ ID NO 9080.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; 008565.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 349 AA;

Query Match 93.4%; Score 1744.5; DB 7; Length 349;
 Best Local Similarity 95.5%; Pred. No. 9.9e-200;
 Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

```

Qy      6 VSIYTS DNYSEE VSGD YDSNKE PCFRDEN VHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      : |||||
Db      1 MEIYTS DNYSEE VSGD YDSNKE PCFRDEN ENFNRI FLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKLR SMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      : |||||
Db     61 GYQKLR SMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVGWIPALLLTIPDFIFADVSQGDIS 185
      : |||||
Db    121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYGVGWIPALLLTIPDIIFADV-----S 175

```

Qy	186	QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKAL	245
Db	176	QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKRKAL	235
Qy	246	KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN	305
Db	236	KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCDFESVVKWISITEALAFFHCCLN	295
Qy	306	PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESSESSSFHSS	359
Db	296	PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESSESSSFHSS	349

Query Match 93.4%; Score 1744.5; DB 10; Length 349;
Best Local Similarity 95.5%; Pred. No. 9.9e-200;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

```

Qy      66 GYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
Db      61 GYQKKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy     126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
Db     121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy     186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
Db     176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 235

Qy     246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
Db     236 KTTVILILAFFACWLPYYVGISIDSFILLEVIVKQGEFESVVKWISITEALAFFHCCLN 295

Qy     306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
Db     296 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 349

```

RESULT 11

AAR68812

ID AAR68812 standard; protein; 352 AA.

XX

AC AAR68812;

XX

DT 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX

DE Human monocyte PF4AR.

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074020_us-10-785-230-3.rup.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074020_us-10-785-230-3.rup.

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GenCore version 6.2
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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:08:15 ; Search time 232 Seconds
(without alignments)
1660.742 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSNDYSEEVGS.....KRGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1867	100.0	359	1	CXCR4_MOUSE	P70658 m c-x-c che
2	1758.5	94.2	349	2	Q8VD47_RAT	Q8vd47 rattus norv
3	1744.5	93.4	349	1	CXCR4_RAT	Q08565 rattus norv
4	1692.5	90.7	352	2	Q7YS92_9EUTH	Q7ys92 tupaia chin
5	1691.5	90.6	352	2	Q8HZU1_CALJA	Q8hzu1 callithrix
6	1689.5	90.5	352	2	Q8HZU0_SAI SC	Q8hzu0 saimiri sci
7	1686.5	90.3	352	1	CXCR4_PAPAN	P56491 papio anubi
8	1679.5	90.0	352	1	CXCR4_MACFA	Q28474 macaca fasc
9	1679.5	90.0	352	2	O77488_CERAE	O77488 cercopithec
10	1678.5	89.9	347	2	Q9MZM9_ATEPA	Q9mzm9 ateles pani
11	1678.5	89.9	352	1	CXCR4_HUMAN	P61073 homo sapien
12	1678.5	89.9	352	1	CXCR4_PANTR	P61072 pan troglod
13	1678.5	89.9	352	2	Q53S69_HUMAN	Q53s69 homo sapien
14	1677.5	89.9	347	2	Q9MZP7_9PRIM	Q9mzp7 presbytis s

15	1676.5	89.8	347	2	Q9MZP5_9PRIM	Q9mzp5	presbytis	p
16	1676.5	89.8	347	2	Q9MZP8_COLPO	Q9mzp8	colobus	pol
17	1676.5	89.8	347	2	Q9MZQ2_PYGRO	Q9mzq2	pygathrix	r
18	1676.5	89.8	347	2	Q9MZQ1_PYGBI	Q9mzq1	pygathrix	b
19	1676.5	89.8	347	2	Q9MZP0_MACAS	Q9mzp0	macaca	assa
20	1676.5	89.8	347	2	Q9MZM5_PITPI	Q9mzm5	pithecia	pi
21	1676.5	89.8	347	2	Q9MZN8_MACTH	Q9mzn8	macaca	thib
22	1676.5	89.8	347	2	Q9MZN7_MACNE	Q9mzn7	macaca	neme
23	1676.5	89.8	347	2	Q9MZP9_NASLA	Q9mzp9	nasalis	lar
24	1676.5	89.8	347	2	Q9MZQ3_PYGAV	Q9mzq3	pygathrix	a
25	1676.5	89.8	347	2	Q9MZQ0_PYGNE	Q9mzq0	pygathrix	n
26	1676.5	89.8	347	2	Q9MZP4_PREFR	Q9mzp4	presbytis	f
27	1676.5	89.8	347	2	Q9MZN9_MACAR	Q9mzn9	macaca	arct
28	1676.5	89.8	347	2	Q9MZM7_CALGO	Q9mzm7	callimico	g
29	1676.5	89.8	352	1	CXCR4_MACMU	P79394	macaca	mula
30	1676.5	89.8	352	2	Q9TSQ8_CERAE	Q9tsq8	cercopithec	
31	1674.5	89.7	347	2	Q9MZM1_EULMA	Q9mzm1	eulemur	mac
32	1674.5	89.7	347	2	Q9MZN0_ALOSE	Q9mzn0	alouatta	se
33	1672.5	89.6	347	2	Q9MZP2_MANSP	Q9mzp2	mandrillus	
34	1672.5	89.6	352	2	Q9BDS5_MACFA	Q9bds5	macaca	fasc
35	1671.5	89.5	347	2	Q9MZN4_HYLLA	Q9mzn4	hylobates	l
36	1670.5	89.5	347	2	Q9MZN2_PONPY	Q9mzn2	pongo	pygma
37	1670.5	89.5	347	2	Q9MZN1_9PRIM	Q9mzn1	gorilla	gor
38	1670.5	89.5	347	2	Q9MZN6_HYLLE	Q9mzn6	nomascus	le
39	1670.5	89.5	347	2	Q9MZN5_BUNHO	Q9mzn5	bunopithec	
40	1670.5	89.5	352	2	Q9BXA0_HUMAN	Q9bxa0	homo	sapien
41	1668.5	89.4	347	2	Q9MZP6_9PRIM	Q9mzp6	presbytis	j
42	1668.5	89.4	347	2	Q9MZM6_CALMO	Q9mzm6	callicebus	
43	1668.5	89.4	347	2	Q9MZP3_SEMEN	Q9mzp3	semnopithec	
44	1668.5	89.4	352	1	CXCR4_CERTO	O62747	cercocebus	
45	1665.5	89.2	347	2	Q9MZN3_HYLSY	Q9mzn3	hylobates	s

ALIGNMENTS

RESULT 1

CXCR4_MOUSE

ID CXCR4_MOUSE STANDARD; PRT; 359 AA.
AC P70658; O09059; O09062; P70233; P70346; Q4KMW1;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 2.
DT 13-JUN-2006, entry version 58.
DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE seven transmembrane domain receptor) (LESTR) (Pre-B-cell-derived
DE chemokine receptor) (PB-CKR) (CD184 antigen).
GN Name=Cxcr4; Synonyms=Cmkar4, Lestr, Sdflr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC STRAIN=129/Sv, and C57BL/6J; TISSUE=Peritoneal exudate;
RX MEDLINE=97113334; PubMed=8955194;
RA Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
RT "Cloning of the mouse fusin gene, homologue to a human HIV-1 co-
RT factor.";
RL J. Immunol. 157:5455-5460(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC TISSUE=Pre-B cell;
RX MEDLINE=97121456; PubMed=8962122; DOI=10.1073/pnas.93.25.14726;
RA Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
RA Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
RT "Molecular cloning and characterization of a murine pre-B-cell growth-
RT stimulating factor/stromal cell-derived factor 1 receptor, a murine
RT homolog of the human immunodeficiency virus 1 entry coreceptor
RT fusin.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC STRAIN=129/Sv; TISSUE=Thymus;
RA Schubel A., Burgstahler R., Lipp M.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS CXCR4-A AND CXCR4-B).
 RC STRAIN=C57BL/6J X CBA; TISSUE=Thymus;
 RX MEDLINE=97439495; PubMed=9295051;
 RA Moepps B., Frodl R., Rodewald H.-R., Baggiolini M., Gierschik P.;
 RT "Two murine homologues of the human chemokine receptor CXCR4 mediating
 RT stromal cell-derived factor 1alpha activation of Gi2 are
 RT differentially expressed in vivo.";
 RL Eur. J. Immunol. 27:2102-2112(1997).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS CXCR4-A AND CXCR4-B).
 RX MEDLINE=97256574; PubMed=9103415;
 RA Heesen M., Berman M.A., Hoepken U.E., Gerard N.P., Dorf M.E.;
 RT "Alternate splicing of mouse fusin/CXC chemokine receptor-4: stromal
 RT cell-derived factor-1alpha is a ligand for both CXC chemokine
 RT receptor-4 isoforms.";
 RL J. Immunol. 158:3561-3564(1997).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM CXCR4-B).
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=99095114; PubMed=9879064;
 RA Frodl R., Gierschik P., Moepps B.;
 RT "Genomic organization and expression of the CXCR4 gene in mouse and
 RT man: absence of a splice variant corresponding to mouse CXCR4-B in
 RT human tissues.";
 RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
 RN [9]
 RP FUNCTION.
 RX MEDLINE=98295994; PubMed=9634237; DOI=10.1038/31261;
 RA Tachibana K., Hirota S., Iizasa H., Yoshida H., Kawabata K.,
 RA Kataoka Y., Kitamura Y., Matsushima K., Yoshida N., Nishikawa S.,
 RA Kishimoto T., Nagasawa T.;
 RT "The chemokine receptor CXCR4 is essential for vascularization of the
 RT gastrointestinal tract.";
 RL Nature 393:591-594(1998).
 RN [10]
 RP FUNCTION.
 RX MEDLINE=98295995; PubMed=9634238; DOI=10.1038/31269;
 RA Zou Y.-R., Kottmann A.H., Kuroda M., Taniuchi I., Littman D.R.;
 RT "Function of the chemokine receptor CXCR4 in haematopoiesis and in
 RT cerebellar development.";
 RL Nature 393:595-599(1998).
 RN [11]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=ICR;
 RX MEDLINE=99410349; PubMed=10479460; DOI=10.1006/dbio.1999.9405;
 RA McGrath K.E., Koniski A.D., Maltby K.M., McGann J.K., Palis J.;

RT "Embryonic expression and function of the chemokine SDF-1 and its
 RT receptor, CXCR4.";
 RL Dev. Biol. 213:442-456(1999).
 CC -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Involved in B-cell lymphopoiesis, bone-marrow myelopoiesis
 CC and in cardiac ventricular septum formation. Plays also an
 CC essential role in vascularization of the gastrointestinal tract,
 CC probably by regulating vascular branching and/or remodelling
 CC processes in endothelial cells. Involved in cerebellar neuronal
 CC layer formation, preventing premature migration of proliferating
 CC granule cells from the external granule layer inwards. In the CNS,
 CC could mediate hippocampal-neuron survival.
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=CXCR4-B; Synonyms=LESTR-B;
 CC IsoId=P70658-1; Sequence=Displayed;
 CC Name=CXCR4-A; Synonyms=LESTR-A;
 CC IsoId=P70658-2; Sequence=VSP_001891;
 CC -!- TISSUE SPECIFICITY: Lymphocytes, macrophages, neutrophils,
 CC microglial cells and astrocytes. Found in spleen, thymus, bone
 CC marrow, lymph nodes and, at lower levels in brain, small
 CC intestine, stomach and kidney. CXCR4-A is predominant in all
 CC tissues tested.
 CC -!- DEVELOPMENTAL STAGE: High expression during embryonic development
 CC does not seem to be associated with the differentiation of any
 CC particular cell type, but is widely utilized when there is a
 CC requirement for cell movement. Frequently associated with less
 CC differentiated cell types and down-regulated with subsequent
 CC differentiation. Detected in sites with haemopoietic potential:
 CC the yolk sac (7.5, 8.5 and 12.5 dpc) and fetal liver (12.5 dpc).
 CC During gastrulation, at 7.2 to 7.8 dpc, expressed in the mesoderm
 CC and the definitive endoderm. As gastrulation pattern fades (8.5
 CC dpc), expression in the mesoderm is down-regulated, while it
 CC becomes predominant in neural ectoderm. Endodermal expression is
 CC retained in the foregut and later in a subset of foregut
 CC derivatives, including the stomach (10.5 dpc), the cystic ducts of
 CC the gall bladder and the lung epithelium (12.5 dpc). In neuronal
 CC tissue: at 10.5 and 12.5 dpc, expressed in the dorsal root
 CC ganglia, in the ventral mantle layer of the spinal cord (or basal
 CC plates), in the hindbrain. At 14.5 dpc, expression more tightly
 CC confined to the neural epithelium lining the ventricular space and
 CC to the external granular layer of the ventral rhombic lip (the
 CC developing cerebellum). Expressed in the outpocketing of the
 CC diencephalic floor at 10.5 dpc and in the developing thalamus and,
 CC to a lesser extent, the developing hypothalamus. At 14.5 dpc,
 CC restricted to the region where thalamus and hypothalamus meet.
 CC Detected in a discrete band of cells at the edge of the olfactory
 CC bulb. In the vascular system: expressed in the endothelium of
 CC numerous blood vessels, but not all, at 10.5, 11.5 and 12.5 dpc,
 CC such as vitelline/umbilical vessels, cardiac ventricular wall
 CC capillaries, facial vessels and, at 14.5 dpc, in the vasculature
 CC of the herniated gut. Expression seems to be associated with
 CC expanding vascular networks. In the heart development, expressed
 CC at 10.5 dpc in the precursor to the aortopulmonary (AP) septum. At
 CC 12.5 dpc, detected in the AP septum at the base of the outflow
 CC tract and in the atrioventricular valves. Detected in craniofacial
 CC ectoderm from 10.5 to 14.5 dpc. At 10.5 and 11.5 dpc, expressed in
 CC the Rathke pouch.
 CC -!- PTM: Sulfated (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U59760; AAB07725.1; -; mRNA.
 DR EMBL; U65580; AAC52953.1; -; Genomic_DNA.
 DR EMBL; D87747; BAA13451.1; -; mRNA.
 DR EMBL; Z80111; CAB02201.1; -; mRNA.
 DR EMBL; Z80112; CAB02202.1; -; mRNA.
 DR EMBL; X99581; CAA67893.1; -; Genomic_DNA.
 DR EMBL; X99582; CAA67894.1; -; mRNA.
 DR EMBL; AB000803; BAA19187.1; -; mRNA.
 DR EMBL; BC031665; AAH31665.1; -; mRNA.
 DR EMBL; BC098322; AAH98322.1; -; mRNA.

DR UniGene; Mm.1401; -.
 DR Ensembl; ENSMUSG00000045382; Mus musculus.
 DR MGI; MGI:109563; Cxcr4.
 DR GO; GO:0030426; C:growth cone; IDA.
 DR GO; GO:0001667; P:ameboidal cell migration; IMP.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0007281; P:germ cell development; IMP.
 DR GO; GO:0008354; P:germ cell migration; IMP.
 DR GO; GO:0008045; P:motor axon guidance; IMP.
 DR GO; GO:0001764; P:neuron migration; IDA.

Query Match 100.0%; Score 1867; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.6e-137;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEPISVSIYTS DNYSEEVGSGDYSDNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
      |||
Db      1 MEPISVSIYTS DNYSEEVGSGDYSDNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60

Qy     61 VILVMGYQKRLRSMTDKYRLHLSVADLLFVITLPFVAVDAMADWYFGKFLCKAVHIIYTV 120
      |||
Db     61 VILVMGYQKRLRSMTDKYRLHLSVADLLFVITLPFVAVDAMADWYFGKFLCKAVHIIYTV 120

Qy    121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 180
      |||
Db    121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 180

Qy    181 QGDISQGD DRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240
      |||
Db    181 QGDISQGD DRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240

Qy    241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
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Db    241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy    301 HCCLNPILYAFLGAKFKSSAQHALNMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db    301 HCCLNPILYAFLGAKFKSSAQHALNMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
  
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RESULT 2
 Q8VD47_RAT
 ID Q8VD47_RAT PRELIMINARY; PRT; 349 AA.
 AC Q8VD47;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 04-APR-2006, entry version 27.
 DE Chemokine receptor CXCR4 (CXC chemokine receptor).
 GN Name=Cxcr4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Holtzman; TISSUE=Whole brain;
 RA Simen A.A., Miller R.J.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 DR EMBL; AF452185; AAL47855.1; -; mRNA.
 DR EMBL; BC089804; AAH89804.1; -; mRNA.
 DR UniGene; Rn.44431; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000355; Chmkine_rcpt.
 DR InterPro; IPR001277; CXC_4_rcpt.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR00645; CXCCHEMOKINER4.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Membrane; Receptor; Transducer;
 KW Transmembrane.
 SQ SEQUENCE 349 AA; 39429 MW; 09D19860D3D2CB8A CRC64;

Query Match 94.2%; Score 1758.5; DB 2; Length 349;
 Best Local Similarity 96.0%; Pred. No. 4.7e-129;
 Matches 340; Conservative 4; Mismatches 5; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       : |||||
Db      1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||
Db     61 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
       |||||
Db    121 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDIIFADV-----S 175

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 245
       |||
Db    176 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 235

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
       |||||
Db    236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGEFESVVKWISITEALAFFHCCLN 295

Qy    306 PILYAFGLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
       |||||
Db    296 PILYAFGLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
  
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RESULT 3
 CXCR4_RAT
 ID CXCR4_RAT STANDARD; PRT; 349 AA.
 AC 008565;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot..

DT 01-JUL-1997, sequence version 1.
 DT 27-JUN-2006, entry version 44.
 DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
 DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
 DE seven transmembrane domain receptor) (LESTR) (CD184 antigen).
 GN Name=Cxcr4; Synonyms=Cmkr4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Wistar; TISSUE=Spleen;
 RA Harrison J.K., Salafranca M.N.;
 RT "Molecular cloning of rat CXCR4.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Involved in B-cell lymphopoiesis, bone-marrow myelopoiesis
 CC and in cardiac ventricular septum formation. Plays also an
 CC essential role in vascularization of the gastrointestinal tract,
 CC probably by regulating vascular branching and/or remodelling
 CC processes in endothelial cells. Involved in cerebellar neuronal
 CC layer formation, preventing premature migration of proliferating
 CC granule cells from the external granule layer inwards. In the CNS,
 CC could mediate hippocampal-neuron survival (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in neurons and in astrocytes.
 CC -!- PTM: Sulfated (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U90610; AAB50408.1; -; mRNA.
 DR Ensembl; ENSRNOG00000003866; Rattus norvegicus.
 DR RGD; 620465; Cxcr4.
 DR GO; GO:0016494; F:C-X-C chemokine receptor activity; TAS.
 DR GO; GO:0001764; P:neuron migration; IDA.
 DR GO; GO:0008038; P:neuron recognition; IEP.
 DR InterPro; IPR000355; Chmkine_rcpt.
 DR InterPro; IPR001277; CXC_4_rcpt.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR00645; CXCHMKINER4.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
 KW Sulfation; Transducer; Transmembrane.
 FT CHAIN 1 349 C-X-C chemokine receptor type 4.
 FT /FTID=PRO_0000069358.
 FT TOPO_DOM 1 36 Extracellular (Potential).
 FT TRANSMEM 37 60 1 (Potential).
 FT TOPO_DOM 61 76 Cytoplasmic (Potential).
 FT TRANSMEM 77 96 2 (Potential).
 FT TOPO_DOM 97 107 Extracellular (Potential).
 FT TRANSMEM 108 129 3 (Potential).
 FT TOPO_DOM 130 151 Cytoplasmic (Potential).
 FT TRANSMEM 152 172 4 (Potential).
 FT TOPO_DOM 173 197 Extracellular (Potential).
 FT TRANSMEM 198 217 5 (Potential).
 FT TOPO_DOM 218 237 Cytoplasmic (Potential).
 FT TRANSMEM 238 258 6 (Potential).
 FT TOPO_DOM 259 282 Extracellular (Potential).
 FT TRANSMEM 283 302 7 (Potential).
 FT TOPO_DOM 303 349 Cytoplasmic (Potential).
 FT MOD_RES 4 4 Sulfotyrosine (Potential).
 FT MOD_RES 18 18 Sulfotyrosine (Potential).
 FT CARBOHYD 8 8 N-linked (GlcNAc...) (Potential).
 FT DISULFID 106 183 By similarity.
 SQ SEQUENCE 349 AA; 39334 MW; 7E0789A605C60C09 CRC64;

Query Match 93.4%; Score 1744.5; DB 1; Length 349;

Best Local Similarity 95.5%; Pred. No. 5.8e-128;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        : |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db      1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db     61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADV SQDIS 185
        ||||||||||||||||||| ||||||||||||||||||| ||||| |
Db    121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYGVWIPALLLTIPDIIFADV-----S 175

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 235

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
        ||||||||||||||||||| ||||||||||||||||||| |||||:|||||
Db    236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFSVVKWISITEALAFFHCCLN 295

Qy    306 PILYAFGLAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSSVSTESESSSFHSS 359
        ||||||||||||||||||| |||||||||||||||||||
Db    296 PILYAFGLAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSSVSTESESSSFHSS 349
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RESULT 4

Q7YS92_9EUTH

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ID Q7YS92_9EUTH PRELIMINARY; PRT; 352 AA.
AC Q7YS92;
DT 01-OCT-2003, integrated into UniProtKB/TreMBL.
DT 01-OCT-2003, sequence version 1.
DT 21-FEB-2006, entry version 16.
DE Chemokine receptor CXCR4.
OS Tupaia chinensis (Chinese tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.
OX NCBI_TaxID=246437;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang M., Ben K.;
RT "Cloning and sequence analysis of HIV-1 related genes of CD4, CXCR4
RT and CCR5 from tree shrew.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY177628; AAO47588.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000355; Chmkine_rcpt.
DR InterPro; IPR001277; CXCR4_rcpt.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00645; CXCCHEMOKINER4.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Membrane; Receptor; Transducer;
KW Transmembrane.
SQ SEQUENCE 352 AA; 39719 MW; 606B07A6D46A7D53 CRC64;
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Query Match 90.7%; Score 1692.5; DB 2; Length 352;
Best Local Similarity 91.2%; Pred. No. 6.8e-124;

Matches 323; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:||||| |||||:| ||||| ||||| ||||| |||||
Db      4 ISIYTSNDYSEELGSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFVAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||||:||||| |||||:| ||||| ||||| ||||| |||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFVAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
       |||||||:||||| |||||:| ||||| ||||| ||||| |||||
Db    124 VLILAFISLDRLAIVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 245
       : ||||||| ||: ||:||||| ||||| ||||| ||||| ||||| |||||
Db    179 EAEDRYICDRFYFNDLWVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
       |||||||:||||| |||||:| ||||| ||||| ||||| ||||| |||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQCFESTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSSVSTESSSSFHSS 359
       ||||||| ||: ||||| ||||| ||||| ||||| ||||| |||||
Db    299 PILYAFILGAKFKSSAQHALTSVSRGSSLKILSKGKRGHSSSVSTESSSSFHSS 352

```

RESULT 5

Q8HZU1_CALJA

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ID   Q8HZU1_CALJA   PRELIMINARY;   PRT;   352 AA.
AC   Q8HZU1;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 19.
DE   Chemokine receptor CXCR4.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Platyrrhini; Cebidae; Callitrichinae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 infection of New World monkey cells occurs
RT   primarily at the stage of virus entry.";
RL   J. Exp. Med. 196:431-445(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AF452612; AAN14528.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CXCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRHRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39803 MW;  8018A4500FC887C0 CRC64;

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Query Match 90.6%; Score 1691.5; DB 2; Length 352;

Qy	6	VSIYTSNDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM	65
Db	4	ISIIYTSNDNYTEEIGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM	63
Qy	66	GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS	125
Db	64	GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSS	123
Qy	126	VLILAFISLDRYLAIVHATNSQRPKRLLAEKAVYVGWVIPALLTIPDFIFADV SQGDIS	185
Db	124	VLILAFISLDRYLAIVHATNSQRPKRLLAEKVYVGWVIPALLTIPDFIFANV-----S	178
Qy	186	QGDDRYICDRLYPDSLWMVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGKHQKRKAL	245
Db	179	EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSGKHQKRKAL	238
Qy	246	KTTVILILAFFACWLPPYYGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN	305
Db	239	KTTVILILAFFACWLPPYYIGISIDSFILLEIIHQGCEFENTVHKWISITEALAFFHCCLN	298
Qy	306	PILYAFLGAKFKSSAQHALNSMSRGSCLKILSKGKRGHSSSVSTESSESSSFHSS	359
Db	299	PILYAFLGAKFKTSAOHALTSVSRGSSCLKILSKGKRGHSSSVSTESSESSSFHSS	352

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ID      Q8HZU0_SAISC      PRELIMINARY; PRT; 352 AA.
AC      Q8HZU0;
DT      01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT      01-MAR-2003, sequence version 1.
DT      30-MAY-2006, entry version 19.
DE      Chemokine receptor CXCR4.
OS      Saimiri sciureus (Common squirrel monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Platyrrhini; Cebidae; Saimiriinae; Saimiri.
OX      NCBI_TaxID=9521;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA      LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT      "Blockade of HIV-1 infection of New World monkey cells occurs
RT      primarily at the stage of virus entry.";
RL      J. Exp. Med. 196:431-445(2002).
CC      -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC      -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR      EMBL; AF452613; AAN14529.1; -; mRNA.
GO      GO:0016021; C:integral to membrane; IEA.
GO      GO:0016020; C:membrane; IEA.
GO      GO:0016493; F:C-C chemokine receptor activity; IEA.
GO      GO:0016494; F:C-X-C chemokine receptor activity; IEA.
GO      GO:0004872; F:receptor activity; IEA.
GO      GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO      GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
GO      GO:0007165; P:signal transduction; IEA.
DR      InterPro; IPR000355; Chmkine_rcpt.
DR      InterPro; IPR001277; CXC_4_rcpt.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00657; CCHEMOKINER.
DR      PRINTS; PR00645; CXCCHEMKINER4.
DR      PRINTS; PR00237; GPCRRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Membrane; Receptor; Transducer;
KW      Transmembrane.
SQ      SEQUENCE 352 AA; 39821 MW; BF1A21FBOC8D4487 CRC64;

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Query Match 90.5%; Score 1689.5; DB 2; Length 352;
 Best Local Similarity 90.7%; Pred. No. 1.2e-123;
 Matches 321; Conservative 18; Mismatches 10; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYSDNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db      4 ISIYTSNDYTEEMGSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSGDIS 185
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db    179 EADDRYICDRFPNDLWVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFGLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSSVSTESESSSFHSS 359
       :|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:|||||||:|:
Db    299 PILYAFGLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSSVSTESESSSFHSS 352
  
```

RESULT 7

CXCR4_PAPAN

```

ID  CXCR4_PAPAN      STANDARD;      PRT;      352 AA.
AC  P56491;
DT  15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT  15-JUL-1998, sequence version 1.
DT  18-APR-2006, entry version 33.
DE  C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE  (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
GN  Name=CXCR4;
OS  Papio anubis (Olive baboon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC  Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
OX  NCBI_TaxID=9555;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [MRNA].
RX  MEDLINE=98346785; PubMed=9683255; DOI=10.1016/S0161-5890(98)00016-9;
RA  Benton P.A., Lee D.R., Kennedy R.C.;
RT  "Sequence comparisons of non-human primate HIV-1 coreceptor
RT  homologues.";
RL  Mol. Immunol. 35:95-101(1998).
CC  -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC  Transduces a signal by increasing the intracellular calcium ions
CC  level (By similarity).
CC  -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC  -!- PTM: Sulfated (By similarity).
CC  -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AF031089; AAC63831.1; -; mRNA.
DR  InterPro; IPR000355; Chmkine_rcpt.
DR  InterPro; IPR001277; CXC_4_rcpt.
DR  InterPro; IPR000276; GPCR_Rhodopsn.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00657; CCCHEMOKINER.
DR  PRINTS; PR00645; CXCCHMKINER4.
DR  PRINTS; PR00237; GPCRRHODOPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW  Sulfation; Transducer; Transmembrane.
FT  CHAIN      1      352      C-X-C chemokine receptor type 4.
FT           /FTId=PRO_0000069357.
FT  TOPO_DOM      1      39      Extracellular (Potential).
  
```

FT	TRANSMEM	40	63	1 (Potential).
FT	TOPO_DOM	64	79	Cytoplasmic (Potential).
FT	TRANSMEM	80	99	2 (Potential).
FT	TOPO_DOM	100	110	Extracellular (Potential).
FT	TRANSMEM	111	132	3 (Potential).
FT	TOPO_DOM	133	154	Cytoplasmic (Potential).
FT	TRANSMEM	155	175	4 (Potential).
FT	TOPO_DOM	176	200	Extracellular (Potential).
FT	TRANSMEM	201	220	5 (Potential).
FT	TOPO_DOM	221	240	Cytoplasmic (Potential).
FT	TRANSMEM	241	261	6 (Potential).
FT	TOPO_DOM	262	285	Extracellular (Potential).
FT	TRANSMEM	286	305	7 (Potential).
FT	TOPO_DOM	306	352	Cytoplasmic (Potential).
FT	MOD_RES	21	21	Sulfotyrosine (Potential).
FT	CARBOHYD	11	11	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	109	186	By similarity.
SQ	SEQUENCE	352 AA;	39752 MW;	468E542E1851265A CRC64;

Query Match 90.3%; Score 1686.5; DB 1; Length 352;
 Best Local Similarity 90.7%; Pred. No. 2e-123;
 Matches 321; Conservative 16; Mismatches 12; Indels 5; Gaps 1;

Qy	6	VSIYTS DNYSEE VSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM	65
Db	4	ISIYTS DNYTEEMSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM	63
Qy	66	GYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS	125
Db	64	GYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFKLCKAVHVIYTVNLYSS	123
Qy	126	VLILAFISLD RYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADV SQGDIS	185
Db	124	VLILAFISLD RYLAIVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFASV-----S	178
Qy	186	QGDDRYICDR LYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKAL	245
Db	179	EADDRYICDR FYPNDLWVVFQFHIMVGLILPGIVILSCYCIISKL SHSKGHQKRKAL	238
Qy	246	KTTVILILAF FACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN	305
Db	239	KTTVILILAF FACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN	298
Qy	306	PILYAF LGA FKFSQAQH ALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS	359
Db	299	PILYAF LGA FKFTSAQH ALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS	352

RESULT 8

CXCR4_MACFA
 ID CXCR4_MACFA STANDARD; PRT; 352 AA.
 AC Q28474;
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1996, sequence version 1.
 DT 18-APR-2006, entry version 35.
 DE C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR) (CD184
 DE antigen).
 GN Name=CXCR4;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Tatsumi M., Takahashi H.;
 RT "Monkey CD4 and fusin are not species barrier for HIV-1 replication.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- PTM: Sulfated (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Membrane (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB015943; BAA31327.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000355; Chmkine_rcpt.
 DR InterPro; IPR001277; CXC_4_rcpt.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR00645; CXCCHEMOKINER4.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details f

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10785230 and Search Result 2007020
start

GenCore version 6.2
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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:15:46 ; Search time 26 Seconds
(without alignments)
1315.579 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSNDYSEEVGS.....KRGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1679.5	90.0	352	2	G00048	fusin (LESTRA) - c
2	1678.5	89.9	352	2	A45747	neuropeptide Y/pep
3	1631	87.4	353	2	S28787	neuropeptide Y/pep
4	585.5	31.4	367	2	JE0349	interferon-inducib
5	570.5	30.6	360	2	A57160	chemokine (C-C) re
6	551.5	29.5	355	2	JQ1231	interleukin-8 rece
7	550.5	29.5	378	2	A55735	G protein-coupled
8	547.5	29.3	356	2	S42096	interleukin-8 rece
9	544.5	29.2	358	2	A53752	interleukin-8 rece
10	544.5	29.2	360	2	A53611	interleukin-8 rece
11	537.5	28.8	378	2	B55735	lymphocyte-specifi
12	535	28.7	369	2	JC5068	G protein-coupled
13	533	28.5	355	2	JC4304	orphan G protein-c
14	530	28.4	360	2	JC4587	chemokine (C-C) re
15	526.5	28.2	327	2	S56162	MDCR15 protein - h
16	523.5	28.0	359	2	A48921	interleukin-8 rece
17	522.5	28.0	350	2	A39445	interleukin-8 rece
18	522.5	28.0	372	2	S26667	G protein-coupled
19	518.5	27.8	378	2	A45680	G protein-coupled

20	517.5	27.7	374	2	S42628	G protein-coupled
21	508.5	27.2	374	2	S32785	G protein-coupled
22	507	27.2	383	2	S55594	G protein-coupled
23	501	26.8	354	2	I58186	probable G protein
24	496	26.6	374	2	I38450	chemokine (C-C) re
25	494	26.5	355	2	JC5067	G protein-coupled
26	484	25.9	350	2	JN0621	G protein-coupled
27	483.5	25.9	352	2	A43113	chemokine (C-C) re
28	479.5	25.7	360	2	JC2443	chemokine (C-C) re
29	476.5	25.5	355	2	G02436	chemokine (C-C) re
30	473.5	25.4	359	2	S15403	angiotensin II rec
31	472.5	25.3	355	2	A45177	chemokine (C-C) re
32	463.5	24.8	359	2	JC1104	angiotensin II rec
33	463.5	24.8	362	2	JN0694	angiotensin II rec
34	460	24.6	362	2	A30341	G protein-coupled
35	459.5	24.6	359	2	S44425	angiotensin II rec
36	459.5	24.6	359	2	JH0621	angiotensin II rec
37	459.5	24.6	359	2	A42656	angiotensin II rec
38	459.5	24.6	359	2	JC2134	angiotensin II rec
39	457.5	24.5	359	2	A48857	angiotensin II rec
40	453.5	24.3	359	2	JQ1516	angiotensin II rec
41	453	24.3	354	2	A23669	interleukin-8 rece
42	448	24.0	362	2	A39714	G protein-coupled
43	447.5	24.0	359	2	I49341	MIP-1 alpha recept
44	445.5	23.9	359	2	I39418	angiotensin II rec
45	442.5	23.7	359	2	JC1194	angiotensin II rec

ALIGNMENTS

RESULT 1

G00048

fusin (LESTRA) - crab-eating macaque

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C;Accession: G00048

R;Tatsumi, M.

submitted to GenBank, July 1996

A;Reference number: H00048

A;Accession: G00048

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-352 <TAT>

A;Cross-references: UNIPROT:Q28474; UNIPARC:UPI0000127302; GB:D86579; NID:g1468948; PID:g1468949

C;Superfamily: vertebrate rhodopsin

Query Match 90.0%; Score 1679.5; DB 2; Length 352;
 Best Local Similarity 90.1%; Pred. No. 3.4e-139;
 Matches 319; Conservative 17; Mismatches 13; Indels 5; Gaps 1;

Qy	6	VSIYTSNDYSEEVSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM	65
		: : : :	
Db	4	ISIYTSNDYTEEMSGDYDSIKEPCFRENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM	63
Qy	66	GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS	125
		: : : : : : :	
Db	64	GYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS	123
Qy	126	VLILAFISLDRLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSGQDIS	185
		: : : : : : :	
Db	124	VLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFASV-----S	178
Qy	186	QGDDRYICDRLYPDSLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL	245
		: : : : : : : :	
Db	179	EADDRYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL	238
Qy	246	KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALFFHCCLN	305
		: : : : : : :	
Db	239	KTTVILILAFFACWLPYYIGISIDSFILLEIKQCFENTVHKWISITEALGFFHCCLN	298
Qy	306	PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESSESSFHSS	359
		: : : : : : :	
Db	299	PILYAFILGAKFKTSAQHALTSVRGSSSLKILSKGKRGGHSSVSTESSESSFHSS	352

RESULT 2

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; receptor D2S201E

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: A45747; A53103; I53006; I59444; I69203; S32761

R;Federspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis, I.; Jirik, F.R. Genomics 16, 707-712, 1993

A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transm

A;Reference number: A45747; MUID:93315164; PMID:8325644

A;Accession: A45747

A;Molecule type: mRNA

A;Residues: 1-352 <FED>

A;Cross-references: UNIPROT:P61073; UNIPARC:UPI000000106C; GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g29

R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocy

A;Reference number: A53103; MUID:94103215; PMID:8276799

A;Accession: A53103

A;Molecule type: mRNA

A;Residues: 1-352 <LOE>

A;Cross-references: UNIPARC:UPI000000106C; EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100

R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A;Title: Molecular cloning, characterization, and localization of the human homolog to the reported bovine

A;Reference number: I53006; MUID:93319629; PMID:8329116

A;Accession: I53006

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <HER>

A;Cross-references: UNIPARC:UPI000000106C; GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928

R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Larhammar, D.; Wahlest Regul. Pept. 47, 247-258, 1993

A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neithe

A;Reference number: I59444; MUID:94052833; PMID:8234909

A;Accession: I59444

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <RE2>

A;Cross-references: UNIPARC:UPI000000106C; GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314

R;Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide rec

A;Reference number: I54751; MUID:94092629; PMID:7505609

A;Accession: I69203

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-352 <RES>

A;Cross-references: UNIPARC:UPI000000106C; GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869

C;Genetics:

A;Gene: GDB:NPY3R; NPY3

A;Cross-references: GDB:230002; OMIM:162643

A;Map position: 2q21-2q21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.9%; Score 1678.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 4.2e-139;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSDNYSSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:|:||||| ||||:| | :|:||||| | ||||| |||||
Db      4 ISIYTSDNYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRLYLAIHVATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSGQDIS 185
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    124 VLILAFISLDRLYLAIHVATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 245
       : ||||| ||: ||: ||||| ||||| ||||| ||||| ||||| |||||
Db    179 EADDRIICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 238
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Qy 246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
 Db 239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy 306 PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGRGGHSSVSTESESSSFHSS 359
 Db 299 PILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 352

RESULT 3

S28787

neuropeptide Y/peptide YY receptor Y3 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: S28787

R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.

Mol. Pharmacol. 40, 869-875, 1991

A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.

A;Reference number: S28787; MUID:92100053; PMID:1661837

A;Accession: S28787

A;Molecule type: mRNA

A;Residues: 1-353 <RIM>

A;Cross-references: UNIPROT:P25930; UNIPARC:UPI00001272FF; EMBL:M86739

C;Superfamily: vertebrate rhodopsin

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 87.4%; Score 1631; DB 2; Length 353;
 Best Local Similarity 86.8%; Pred. No. 5.9e-135;
 Matches 308; Conservative 26; Mismatches 15; Indels 6; Gaps 2;

Qy 6 VSIYTSNDYSE-EVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILV 64
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 4 IRIFTSNDYTEDDLGSGDYDSMKEPCFRENAHFNRIFLPTVYSIIFLTGIVGNGLVILV 63

Qy 65 MG YQKKLRSM TD KYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIYTVNLYS 124
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 64 MG YQKKLRSM TD KYRLHLSVADLLFVLTLPFWAVDAVANWYFGKFLCKAVHIYTVNLYS 123

Qy 125 SVLILAFISLDRYLAI V HATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSQGDI 184
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 124 SVLILAFISLDRYLAI V HATNSQKPRKLLAEKVYVGWLPVLLTIPDLIFA-----DI 178

Qy 185 SQGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCI I I SKLSHSGHKQRKA 244
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 179 KEVDERYICDRFYPSDLWL V VFQFQHIVGLLLP GIVILSCYCI I I SKLSHSGKYQKRKA 238

Qy 245 L KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCL 304
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 239 L KTTVILIL T FFACWLPYYIGISIDSFILLEI I QGCEFESTVHKWISITEALAFFHCCL 298

Qy 305 NPILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGRGGHSSVSTESESSSFHSS 359
 : :|||||:| :||||| ||||||:| ||||||:| ||||||:| |
 Db 299 NPILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGRGGHSSVSTESESSSFHSS 353

RESULT 4

JE0349

interferon-inducible protein 10 (IP-10) receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C;Accession: JE0349

R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.

Biochem. Biophys. Res. Commun. 251, 41-48, 1998

A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its specific expression

A;Reference number: JE0349; MUID:99009219; PMID:9790904

A;Accession: JE0349

A;Molecule type: mRNA

A;Residues: 1-367 <TAM>

A;Cross-references: UNIPROT:Q9QWN6; UNIPARC:UPI0000029B69; DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PI

C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.

C;Superfamily: vertebrate rhodopsin

Query Match 31.4%; Score 585.5; DB 2; Length 367;
 Best Local Similarity 35.4%; Pred. No. 1.5e-43;
 Matches 123; Conservative 69; Mismatches 130; Indels 25; Gaps 7;

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Qy      17 EVGSGDYD-SNKEPCFRDENVHFNRIPLPTIYFIIFLTGIVGNGLVILVMGYQKKLRSM 75
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      28 DYGENESDFSDSPPCQDFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSST 87

Qy      76 DKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLD 135
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      88 DTFLLHLAVADVLLVTLPLWAVDAAVQWVFGPGLCKVAGALFNINFYAGAFLLACISFD 147

Qy     136 RYLAIVHATNSQR--PRKLLAEKAVYVGVWIPALLTIPDFIFADVSQGDISQDDRYI- 192
       | | : | | | | | | | : | : | : | : | : | : | : | : | : |
Db     148 RYLSIVHATQIYRRDPRVRVALTCIV--VWGLCLLFALPDFIY-----LSANYDQRLN 198

Qy     193 ---CDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQKALKTTV 249
       | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     199 ATHCQYNFP-QVGRTALRVQLVAGFLLPLVMAYCYAHILAVLLVSRGQRRFRAMRLVV 257

Qy     250 ILILAFFACWLPPYVVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPILY 309
       : : : | | | : : : | : : | : | : | : | : | : | : | : |
Db     258 VVVAFAVACWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLY 317

Qy     310 AFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSF 356
       | : | : | : | : | : | : | : | : | : | : | : | : |
Db     318 AFVGVKFREQMWMLFTRLGRSD-----QRGPQRQPSRSSRESSW 356

```

RESULT 5

```

A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human bas
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; UNIPARC:UPI000002DFE9; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g9
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

```

```

Query Match      30.6%; Score 570.5; DB 2; Length 360;
Best Local Similarity 37.4%; Pred. No. 3.1e-42;
Matches 120; Conservative 63; Mismatches 125; Indels 13; Gaps 6;

```

```

Qy      1 MEPISVSIYTSNDYSEEVGSGD--YDSNKEPCFRDENVHFNRIPLPTIYFIIFLTGIVGN 58
       | | : : | | | : | | : | : | : | : | : | : | : |
Db      1 MNPTDIADTTLD---ESIYSNYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVGLLGN 57

Qy     59 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIY 118
       | : | : | : | : | : | : | : | : | : | : | : | : |
Db     58 SVVVLVLFKYKRLRSMTDVYLLNLAISDLLFVFSLPFWGYAADQWVFGGLGLCKMISWMY 117

Qy     119 TVNLYSSVLILAFISLDYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLTIPDFIFAD 178
       | | : : | : | : | : | : | : | : | : | : | : | : |

```


C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C;Accession: A55735
 R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
 Genomics 23, 643-650, 1994
 A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
 A;Reference number: A55735; MUID:95154835; PMID:7851893
 A;Accession: A55735
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-378 <SCH>
 A;Cross-references: UNIPROT:P47774; UNIPARC:UPI00000274D1; GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g46
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 29.5%; Score 550.5; DB 2; Length 378;
 Best Local Similarity 33.2%; Pred. No. 1.8e-40;
 Matches 117; Conservative 78; Mismatches 150; Indels 7; Gaps 3;

```

Qy      11 SDNYSEEVSGDYSNKEPCFRDENVHFNRIFLTPTIYFIIFLTGIVGNGLVILVMGYQKK 70
          :|:| | : || : ||: : :| ||| :| :| |::| |||| | |:
Db      29 TDDYIGENTTVDTLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKR 88

Qy      71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
          |::|| | |::|::|::| |||| | || :|| : || :: :| :|:|
Db      89 LKTMTDTYLLNLAVADILFLLILPFWAYSEAKSWIFGVYLCCKGIFGIYKLSFFSGMLLLL 148

Qy     131 FISLDRLAIVHAT--NSQRPRKLLAEKAVYGVWIPALLTIPDFIFADVSQGDISQGD 188
          ||::||:| | : | | || | ||::| | |::| : : : : : |:
Db     149 CISIDRYAIVQAVSRHRHRARVLLISKLSVGIWMLALFLSIPELLYSGLQK---NSGE 205

Qy     189 DRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKALKTT 248
          | | : : : | : : | : : | : : | | || | : : : ||:|
Db     206 DTLRCSLVSAQVEALITIQAQMVFGFLVPMAMSFCYLIIRTLQARNFERNKAIVKI 265

Qy     249 VILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPIL 308
          : :: : | : || : : : : : : : : : : | : | | : | |
Db     266 IAVVVVFIVFQLPYNGVVLAAQTVANFNITNSSCETSKQLNIAVDVYSLASVRCCVNPFL 325

Qy     309 YAFLGAKFKSSAQHALNSMSRGSS--LKILSKGKRGGHSSVSTESSESSSFHS 358
          |||:| ||:| : | | : | : : ||| |::: |
Db     326 YAFIGVKFRSDLFKFLKDLGCLSQERLRHWSSCRHVRNASVSMEAETTTTFS 377
  
```

RESULT 8

S42096
 interleukin-8 receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
 C;Accession: S42096
 R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
 submitted to the EMBL Data Library, February 1994
 A;Description: Molecular cloning of the rat IL8 receptor.
 A;Reference number: S42096
 A;Accession: S42096
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-356 <GOB>
 A;Cross-references: UNIPARC:UPI00001778DE; EMBL:X77797
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.3%; Score 547.5; DB 2; Length 356;
 Best Local Similarity 34.8%; Pred. No. 3.1e-40;
 Matches 129; Conservative 67; Mismatches 124; Indels 51; Gaps 11;

```

Qy      12 DNYS-EEVSGDYG-----SNKEPCFRDENVHFNRIFLTPTIYFIIFLTGIVGN 58
          ||:| | : || | | : | | | : | | : | : | : ||
Db      7 DNFSLDFEFGSDIDSYNFSSDPPFTLSDAAPC-PSANLDINRYAVVVIIYVLVTLVSLVGN 65

Qy     59 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIY 118
          ||::| : | : |::| | |::| | |::| | : | | ||| :
Db     66 SLVMLVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQ 125

Qy     119 TVNLYSSVLILAFISLDRLAIVHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIFAD 178
          : ||||:| |::| |||||::: : : | | : : | :|::| | |
Db     126 EITFYSSVLLLACISMDRYLAIVHATSTLIQKRHLV-KFVCITMWFLSLVLSLPIFIL-- 182
  
```

```

Qy      179 VSQGDISQDDRYICDRLYPD-----SLWMVVFQFQHIMVGLILPGIVILSCYCIISKL 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      183 --RTTVKANPSTVVC---YENIGNNTSKWRVVLRLPQTYGFLPLLLIMLCYGFTRLTL 237

Qy      234 SHSKGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISI 293
      : | | : : : : : : | | | | : : | : : : | | : : : |
Db      238 FKAHMGQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINK---A 294

Qy      294 TEALAFFHCCLNPILYAFLGAKFKSSAQHALNSMSRGSLSKILSK-----GKRGGH 344
      : | | | | | | | | | | | | : | | | | | : : : | |
Db      295 SEILGFLHSCCLNPILYAFIGQKFR----HGL-----LKIMANYGLVSKEFLAKEGRP 342

Qy      345 SSVSTESESS 355
      | : | : : |
Db      343 SFVGSSSANTS 353

```

RESULT 9
A53752

interleukin-8 receptor (clone 5B1a) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53752
R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.
J. Biol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MUID:94230294; PMID:8175642
A;Accession: A53752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
A;Cross-references: UNIPROT:P35344; UNIPARC:UPI000012D4F4; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g43
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.2%; Score 544.5; DB 2; Length 358;
Best Local Similarity 34.7%; Pred. No. 5.7e-40;
Matches 128; Conservative 70; Mismatches 132; Indels 39; Gaps 9;

```

Qy      9 YTSNDYSEEVGSGDYDS-----NKEPCFRDENVHFNRIFLPTIYFIIFLTGIV 56
      : | : | | | | : : : : : : | | | : : | : : | : :
Db      4 FTWENYSYEDFFGDFSNSYSTDLPTLLDSAPC-RSESLETNSYVVLITYILVFLSL 62

Qy      57 GNLVILVMGYQKKLRSMSTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHI 116
      | | | | : | : | : | | | : : | | | : | | | | :
Db      63 GNSLVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSL 122

Qy      117 IYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLTIPDFIF 176
      : | | | : | : | | | | | | : : | | : : : | : | : : |
Db      123 VKEVNFYSGILLACISVDYLAIVHATRTMIQKRHLV-KFICLSMWGVSILSLPILLF 181

Qy      177 ADVSQGDISQDDRYICDRLYPD-----SLWMVVFQFQHIMVGLILPGIVILSCYCIIS 231
      : | : : : : | | : : : | | | : | | | :
Db      182 RNA----IFPPNSSPVC---YEDMGNSTAKWRMVLRLPQTFGFILPLVLMFCYVFTLR 234

Qy      232 KLSHSKGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWI 291
      | : | | : : : : : | | | | : : | : : | : : : :
Db      235 TLFAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRAL 294

Qy      292 SITEALAFFHCCLNPILYAFLGAKF-----KSSAQHALNSMSRGSLSKILSKGKRGGHSS 346
      | | | | | | | | | | | | | | | | | | | | : | : |
Db      295 DATEILGFLHSCCLNPILYAFIGQKFRYGLLKILAAHGL-----ISKEFLAKESR--PSF 346

Qy      347 VSTESESS 355
      | : | : : |
Db      347 VASSGNTS 355

```

RESULT 10
A53611

interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

C;Species: Homo sapiens (man)
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C;Accession: B55735; S52443
 R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W. Genomics 23, 643-650, 1994
 A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
 A;Reference number: A55735; MUID:95154835; PMID:7851893
 A;Accession: B55735
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-378 <SCH>
 A;Cross-references: UNIPROT:P32248; UNIPARC:UPI0000001C2F; GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g46
 R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
 submitted to the EMBL Data Library, February 1995
 A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transactivated by Epstein
 A;Reference number: S52443
 A;Accession: S52443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 21-378 <BUR>
 A;Cross-references: UNIPARC:UPI000014DEAD; EMBL:X84702
 C;Genetics:
 A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
 A;Cross-references: GDB:342065; OMIM:600242
 A;Map position: 17q12-17q21.2
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 28.8%; Score 537.5; DB 2; Length 378;
 Best Local Similarity 32.1%; Pred. No. 2.5e-39;
 Matches 113; Conservative 79; Mismatches 153; Indels 7; Gaps 3;

```

Qy      11 SDNYSEEVSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKK 70
       :|:| : : || : | : : :| ||| :| || |::|||::| | |:
Db      29 TDDYIGDNTTVDTLTFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYYIFKR 88

Qy      71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
       |::||| | |::|::|::|::|::| | | || || : || :: :| :|:|
Db      89 LKTMDDTYLLNLAVADILFLLTLPFWAYSAAKSWWVFGVHFCKLIFAIYKMSFFSGMLLLL 148

Qy      131 FISLDRLYLAIHVHATNS--QRPRKLLAEKAVYGVGWIPALLLTIPDFIFADVSGQDISQGD 188
       ||::||::||| | : : | || | | ||::|| | :|::|: ::|: : | :
Db      149 CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQR---SSSE 205

Qy      189 DRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKALKTT 248
       | : : | : :| :| : : || :|| | : : : : ||:|
Db      206 QAMRCSLITEHVEAFITIQVQMVGIFLVPLLAMSFCYLVIIRTLQARNFERNKAIVKI 265

Qy      249 VILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLNPIL 308
       : : : | ||| : : : | : : : :| :|| ||:| | |
Db      266 IAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFL 325

Qy      309 YAFLGAKFKSSAQHALNSMS--RGSSLKILSKGRGGHSSVSTESSESSSFHS 358
       |||:| ||:: : : | : | : ||:| |:::| |
Db      326 YAFIGVKFRNDLFKLFKDLGCLSQEQLRWSSCRHIRRSSMSVEAETTTTFS 377

```

RESULT 12
 JC5068
 G protein-coupled receptor CKR-L3 - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C;Accession: JC5068
 R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G. Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.
 A;Reference number: JC5067; MUID:97040707; PMID:8886020
 A;Accession: JC5068
 A;Molecule type: DNA
 A;Residues: 1-369 <ZAB>
 A;Cross-references: UNIPARC:UPI0000043586; EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
 C;Comment: This protein belongs to the family of alpha chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
 A;Cross-references: GDB:5370639; OMIM:601835
 A;Map position: 6q27-6q27

C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;42-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;160-180/Domain: transmembrane #status predicted <TM4>
 F;212-233/Domain: transmembrane #status predicted <TM5>
 F;250-271/Domain: transmembrane #status predicted <TM6>
 F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 535; DB 2; Length 369;
 Best Local Similarity 33.9%; Pred. No. 4e-39;
 Matches 124; Conservative 72; Mismatches 136; Indels 34; Gaps 9;

```

Qy      10 TSDNYSEEVGSGDY--DSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 67
       :|::| | : | || | | |::|:| | : |::|| |:: :
Db      9 SSEDFVSVNTSYYSVDSEMLLCSLQEVQRSLFVPIAYSILICVFGLLGNILVVITFAF 68

Qy      68 QKKLRSMTDKYLHLHLSVADLLFVITLPFWAVD-AMADWYFGKFLCKAVHIIYTVNLYSSV 126
       || ||||| | |:::|:|:|:|:|:| | | | | | : || : |
Db      69 YKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGM 128

Qy      127 LILAFISLDRYLAIVHATNS--QRPRKLLAEKAVYGVWIPALLTIPDFIFADVSQGDI 184
       |:| |::|:|:|:| | | | | : : || :::: |:| :|
Db      129 LLTLCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSTFVF---NQKYN 185

Qy      185 SQGDDRYICDRLY----PDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGKHQ 240
       :|| | :|: | | : : : | : | : : || | : | : :
Db      186 TQGS--VCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIICYTFIVKTLVQAQNSK 243

Qy      241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
       : |::: : :| | || :|: : : : | | : : | | : : : || |||
Db      244 RHKAIRVIAVVLVFLACQIPHNMVLLVTA-ANLGKMNRSQCSEKLIGYTKTVTEVLAFL 302

Qy      301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSLSKILS-----KGKRGHSSSVSTES 353
       |||||:|:|:| | | | | | | | | | | | | | | |
Db      303 HCCLNPNVLYAFIGQKF-----RNYFLKILKDLWCVRVKYKSSGFSAGRYSEN 350

Qy      354 SSFHSS 359
       | :|
Db      351 ISRQTS 356

```

RESULT 13

JC4304

orphan G protein-coupled receptor - human

N;Alternate names: V28 protein

C;Species: Homo sapiens (man)

C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C;Accession: JC4304

R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine

A;Reference number: JC4304; MUID:96011651; PMID:7590284

A;Accession: JC4304

A;Molecule type: mRNA

A;Residues: 1-355 <RAP>

A;Cross-references: UNIPROT:P49238; UNIPARC:UPI000000A0B; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g66

A;Experimental source: peripheral blood mononuclear cell

C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces th

C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between

C;Genetics:

A;Gene: v28

A;Map position: 3pter-p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein

F;35-57/Domain: transmembrane #status predicted <TM1>

F;66-88/Domain: transmembrane #status predicted <TM2>

F;104-125/Domain: transmembrane #status predicted <TM3>

F;146-165/Domain: transmembrane #status predicted <TM4>

F;197-217/Domain: transmembrane #status predicted <TM5>

F;230-254/Domain: transmembrane #status predicted <TM6>

F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.5%; Score 533; DB 2; Length 355;
 Best Local Similarity 33.1%; Pred. No. 5.7e-39;

Matches 120; Conservative 65; Mismatches 146; Indels 32; Gaps 7;

Qy 12 DNYSEEVGSG-DYDSNKEPCFRDENVHFNRIPLTIYFIIFLTGIVGNGLVILVMGYQKK 70
| : | | : | | : | | : | | : | | : | | : | | : | |
Db 2 DQFPESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKK 61

Qy 71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
: | : | | | : | : | : | | | | | | : : : | | : : : | : :
Db 62 PKSVTDIYLLNLALSDDLFLVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFIT 121

Qy 131 FISLDRYLAIIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSQGDISQGDDR 190
| : | | | | | | | | | : : : | | | : | : | | : :
Db 122 VISIDRYLAIVLAANSMMNRTVQHGVTISLGVWAAAILVAAPQFMFTKQKENE----- 174

Qy 191 YICDRLYPD---SLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKT 247
| | : : | : : : | : | : : | | | | | | : | : | : |
Db 175 --CLGDYPEVLQEIWPVLRNVETNFLGFLPLLIMSICYFRIIQTLSCKNHHKAKAIKL 232

Qy 248 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPI 307
: : : : | | | | | : : | | : : | : | : | | | : | :
Db 233 ILLVVIVFFLFWTPYNMIFLETCLKYDFF-PSCDMRKDLRLALSVTETVAFSHCCLNPL 291

Qy 308 LYAFLGAKFKSSAQHALNSMRGSSSLKIL-----SKGKRGGHSSSVSTESESSSF 356
: | | | | : | : | : | : | : | : | : | : | : : :
Db 292 IYAFAGEKFRRYLYHLY-----GKCLAVLCGRSVHVDSSSESQRSRHGSVL--SSNFTY 344

Qy 357 HSS 359
| : |
Db 345 HTS 347

RESULT 14

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.

Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human C

A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587

A;Molecule type: mRNA

A;Residues: 1-360 <HOO>

A;Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:

A;Experimental source: thymus

C;Genetics:

A;Gene: cc ckr-4

C;Superfamily: vertebrate rhodopsin

C;Keywords: glycoprotein; phosphoprotein; receptor; thymus

F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 28.4%; Score 530; DB 2; Length 360;

Best Local Similarity 36.4%; Pred. No. 1.1e-38;

Matches 108; Conservative 62; Mismatches 119; Indels 8; Gaps 4;

Qy 23 YDSNKEPCFRDENVHFNRIPLTIYFIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHL 82
| : | : | : : | : | | : | : | : | : | : | : | : | : |
Db 22 YESMPKPCTKEGKAFGEVFLPPLYSVLFLGLFGNSVVVLVLFKYKRLKSMTDVYLLNL 81

Qy 83 SVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLDRYLAIHV 142
: : : | | | : | | | | | : | | : : : : | : | | | | |
Db 82 AISDLLFVLSLPFWGYAADQWVFLGLCKIVSWMYLVGFYSGIFFIMLSIDRYLAIVH 141

Qy 143 ATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSQGDISQGDDRYICDRLYP--DS 200
| | : | | : | : : | : : : : : : | | :
Db 142 AVFSLKARTLTGYVITSLITWSVAVFASLPGLLFSTC----YTEHNHTY-CKTQYSVNST 196

Qy 201 LWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKALKTTVILILAFFACWL 260
| : : : : | : | : | | | : | : : : : : : | : |
Db 197 TWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQCHKNEKNRAVRMIFGVVVLFLGFWT 256

Qy 261 PYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPIYAFGLGAKFK 317

Db 257 PYNVVLFLFETLVELEVL-QDCTLERYLDYAIQATETLGFHCCCLNPVIYFFFLGKFR 312

RESULT 15

S56162

MDCR15 protein - human

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C;Accession: S56162

R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.

Biochem. J. 309, 773-779, 1995

A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript forma

A;Reference number: S56162; MUID:95366951; PMID:7639692

A;Accession: S56162

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-327 <BAR>

A;Cross-references: UNIPARC:UPI000016AD1F; EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784

C;Superfamily: vertebrate rhodopsin

Query Match 28.2%; Score 526.5; DB 2; Length 327;
Best Local Similarity 34.6%; Pred. No. 1.9e-38;
Matches 111; Conservative 66; Mismatches 139; Indels 5; Gaps 4;

Qy 38 FNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWA 97
| :|:| | :|| |::|| ||::: : || | : : ||:|||| | |||
Db 4 FKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLHLAVADLLLVFILPFAV 63

Qy 98 VDMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKA 157
: | | |||| | :: || | | :|| | :||||||| :| | :||
Db 64 AEGSVGWVLGTFLCKTVIALHKVNFCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHI 123

Qy 158 VYGVWIPALLLTIPDFIFADVSGQDISQGDDR--YICDRLYPDSLWMVVFQFQHIMVGL 215
:|: || :|: :|| ||| : | : : | : : : |
Db 124 TCGTIWLVGFLALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWF-TSRFLYHVAGF 182

Qy 216 ILPGIVILSCYCIISKLSHSHKGH-QKRKALKTTVILILAFFACWLPPYVGISIDSFILL 274
:|| :|: || :: :| :: |::||:: :: : || || ||: | :| : |
Db 183 LLPMLVMGWCYVGVVHRLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLRL 242

Qy 275 GVIKQGCDFESIVHKWISITEALAFFHCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLK 334
: | : : |:: | | |||||:| | | ||: | : |
Db 243 KAVDNTCKLNGSLPVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTSPAS 302

Qy 335 ILSKGKRGHSSVSTESESSS 355
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Db 303 LCQLFPSWRRSSLS-ESENAT 322

Search completed: February 6, 2007, 14:23:55
Job time : 27.256 secs

start

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074028_us-10-785-230-3.rai.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
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This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074028_us-10-785-230-3.rai.

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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:23:25 ; Search time 39 Seconds
(without alignments)
808.237 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSIDNYSEEVGS.....KRGHSSVSTESSESSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1678.5	89.9	352	1	US-08-202-056-3	Sequence 3, Appli
2	1678.5	89.9	352	1	US-08-076-093A-4	Sequence 4, Appli
3	1678.5	89.9	352	1	US-08-701-265-4	Sequence 4, Appli
4	1678.5	89.9	352	1	US-08-284-586-4	Sequence 4, Appli
5	1678.5	89.9	352	1	US-08-805-478-4	Sequence 4, Appli
6	1678.5	89.9	352	1	US-08-802-627A-4	Sequence 4, Appli
7	1678.5	89.9	352	1	US-08-801-238-4	Sequence 4, Appli
8	1678.5	89.9	352	1	US-08-801-228-4	Sequence 4, Appli
9	1678.5	89.9	352	2	US-09-104-296-4	Sequence 4, Appli

10	1678.5	89.9	352	2	US-09-517-605-4	Sequence 4, Appli
11	1678.5	89.9	352	2	US-09-647-501-2	Sequence 2, Appli
12	1672.5	89.6	352	2	US-09-826-509-485	Sequence 485, App
13	1641.5	87.9	352	1	US-08-450-393A-6	Sequence 6, Appli
14	1641.5	87.9	352	2	US-08-446-669-6	Sequence 6, Appli
15	1641.5	87.9	352	2	US-09-625-573-6	Sequence 6, Appli
16	1641.5	87.9	352	5	PCT-US95-00476-6	Sequence 6, Appli
17	1621.5	86.9	337	1	US-08-153-848-46	Sequence 46, Appl
18	1621.5	86.9	337	2	US-09-299-843A-46	Sequence 46, Appl
19	1621.5	86.9	337	2	US-09-088-337B-46	Sequence 46, Appl
20	1621.5	86.9	337	5	PCT-US93-11153-46	Sequence 46, Appl
21	584	31.3	368	2	US-08-709-838-2	Sequence 2, Appli
22	584	31.3	368	2	US-08-829-839-2	Sequence 2, Appli
23	584	31.3	368	2	US-09-170-496D-20	Sequence 20, Appl
24	584	31.3	368	2	US-09-624-594-2	Sequence 2, Appli
25	584	31.3	368	2	US-09-607-156-2	Sequence 2, Appli
26	584	31.3	368	3	US-09-633-541-2	Sequence 2, Appli
27	580	31.1	368	2	US-09-170-496D-174	Sequence 174, App
28	570.5	30.6	360	2	US-08-875-573-20	Sequence 20, Appl
29	570.5	30.6	360	2	US-09-232-878-2	Sequence 2, Appli
30	570.5	30.6	360	2	US-09-045-583-55	Sequence 55, Appl
31	570.5	30.6	360	2	US-09-534-185-55	Sequence 55, Appl
32	570.5	30.6	360	2	US-08-939-107-34	Sequence 34, Appl
33	570.5	30.6	360	2	US-10-039-659A-16	Sequence 16, Appl
34	570.5	30.6	360	2	US-09-067-447B-34	Sequence 34, Appl
35	570.5	30.6	360	2	US-09-837-446-2	Sequence 2, Appli
36	570.5	30.6	360	2	US-09-764-413-20	Sequence 20, Appl
37	570.5	30.6	360	2	US-09-796-744-17	Sequence 17, Appl
38	570.5	30.6	360	3	US-09-509-165A-34	Sequence 34, Appl
39	565.5	30.3	123	2	US-08-513-974B-330	Sequence 330, App
40	558.5	29.9	360	2	US-08-833-752-10	Sequence 10, Appl
41	558.5	29.9	360	2	US-09-938-719-10	Sequence 10, Appl
42	558.5	29.9	360	2	US-09-939-226B-10	Sequence 10, Appl
43	558.5	29.9	360	2	US-09-938-703B-10	Sequence 10, Appl
44	550.5	29.5	378	2	US-09-299-843A-66	Sequence 66, Appl
45	550.5	29.5	378	2	US-09-088-337B-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1

US-08-202-056-3

; Sequence 3, Application US/08202056

; Patent No. 5440021

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Hebert, Caroline

; APPLICANT: Kim, Kyung Jin

; APPLICANT: Lee, James

; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/202,056

; FILING DATE: 25-FEB-1994

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: 706P3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-202-056-3

Query Match 89.9%; Score 1678.5; DB 1; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.1e-132;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||||:|||||||:|||||||:|:||||| |||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWVWPALLLTIPDFIFADV SQGDIS 185
        |||||||:|||||||:||||||| |||||:|||||||:| |
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGWVWPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
        : ||||||| |: ||:||||||| |||||:||||||| |||||:|||||||
Db    179 EADDRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        |||||||:|||||||:||||||| :|||||:|: |||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359
        |||||||:||||| |:||||||| |||||:|||||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352
  
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RESULT 2
 US-08-076-093A-4
 ; Sequence 4, Application US/08076093A
 ; Patent No. 5543503
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Lee, James
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Jin Kim, K.
 ; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/076,093A
 ; FILING DATE: 11-Jun-1993
 ; CLASSIFICATION: 530.
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/810782
 ; FILING DATE: 19-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; FILING DATE: 29-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: 706P2

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-076-093A-4
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Query Match      89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;
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Qy      6 VSIYTSNDYSEEVGSGDYSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:|:||||||| |||||:| :|:||||||| |||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||||||:|||||||:|||||||:|:||||| |||||:|||||||
Db     64 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIHVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
       |||||||||:|||||||:|||||||:|||||||:| |||||
Db    124 VLILAFISLDRYLAIHVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
       : ||||||| ||: ||:|||||||:|||||||:|||||||:|||||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
       |||||||||:|||||||:|||||||:|||||||:| |||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFGLAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSVSTESESSSFHSS 359
       |||||||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFGLAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352
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RESULT 3

US-08-701-265-4

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; Sequence 4, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
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Query Match 89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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RESULT 4
US-08-284-586-4
; Sequence 4, Application US/08284586
; Patent No. 5840856
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-284-586-4

```

```

Query Match      89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVSGDYDSNKEPCFRDENVHFNRIFLTPTIYFIIFLTGIVGNGLVILVM 65
        :|||||||:|:||||||| ||||||:| :|:||||||| ||||||||
Db      4 ISIYTSNDYTEEMSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        ||||||||:|:||||||| ||||||:| :|:||||||| ||||||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
        ||||||||:|:||||||| ||||||:| :|:||||||| ||||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
        : ||||||| |: |:||||||| ||||||:| :|:||||||| ||||||||
Db    179 EADDRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCFESIVHKWISITEALAFFHCCLN 305
        ||||||||:|:||||||| :|||||:|: ||||||||:|: |
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSSVSTESSESSFHSS 359
        ||||||||:|:||||| |:||||||| |
Db    299 PILYAFILGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSSVSTESSESSFHSS 352

```

```

RESULT 5
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-805-478-4

```

```

Query Match      89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVGSGDYSDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:|:||||||| |||||:| :|:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||||:|||||||:|||||||:|:||||| |||||:|||||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
       |||||||:|||||||:|||||||:|||||||:|||||||:|
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 245
       : ||||||| |: |:|||||||:|||||||:|||||||:|||||||
Db    179 EADDRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDIESIVHKWISITEALAFFHCCLN 305
       |||||||:|||||||:|||||||:|||||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESSESSFHSS 359
       |||||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFILGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESSESSFHSS 352

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RESULT 6

US-08-802-627A-4

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; Sequence 4, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-802-627A-4

```

```

Query Match      89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSGQDIS 185
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    179 EADDRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDVESIVHKWISITEALAFFHCCLN 305
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352

```

RESULT 7

US-08-801-238-4

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; Sequence 4, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997

```

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-238-4

```

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Query Match      89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      :|||||||:|:||||||| |||||:| | :|:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPEWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPEWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
      |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
      : ||||| | | : | : ||||| |||||:|||||||:|||||||:|||||||
Db    179 EADDRYICDRFYPNLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPPYVIGISIDSFILLGVIKQGCGDFESIVHKWISITEALAFFHCCLN 305
      |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    239 KTTVILILAFFACWLPPYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLLGAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSVSTESESSSFHSS 359
      |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFLLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 8

US-08-801-228-4

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; Sequence 4, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

```



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-4

```

```

Query Match          89.9%; Score 1678.5; DB 1; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||||:|:||||||| |||||:| | :|:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRLAIVHATNSQRPRKLLAEKAVVYGVWIPALLLTIPDFIFADVSQGDIS 185
       |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    124 VLILAFISLDRLAIVHATNSQRPRKLLAEKVYVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
       : ||||| | | : | | : ||||| ||||| ||||| ||||| ||||| |||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDVFESIVHKWISITEALAFFHCCLN 305
       |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFGLGAKFKSSAQHALNMSRGSLSKILSKGKRGGHSSVSTESSESSFHSS 359
       |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFGLGAKFKTSAQHALTSVSRGSLSKILSKGKRGGHSSVSTESSESSFHSS 352

```

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RESULT 9
US-09-104-296-4
; Sequence 4, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-104-296-4

```

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Query Match      89.9%; Score 1678.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||:|:||||| ||||:| :|:||||| |||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFRENNANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       |||||:|||||:|||||:|:| |||||:|||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRLKLLAEKAVYGVWIPALLLTIPDFIFADV SQGDIS 185
       |||||:|||||:|||||:|:| |||||:|||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRLKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
       : ||||| ||: ||:|||||:|||||:|:| |||||
Db    179 EADDRYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFFHCCLN 305
       |||||:|||||:|||||:|:| |||||:|||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEI IKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFGLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359
       |||||:|||||:|||||:|:| |||||:|||||
Db    299 PILYAFGLGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSVSTESESSSFHSS 352

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RESULT 10

US-09-517-605-4

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; Sequence 4, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02

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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-4

Query Match 89.9%; Score 1678.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||:|:||||| |||||:| :|:||||| |||||:|||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSGQDIS 185
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
        : ||||| ||: ||:|||||:|||||:|||||:|||||:|||||:|||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSIFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    239 KTTVILILAFFACWLPYYIGISIDSIFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESSESSFHSS 359
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Db    299 PILYAFILGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESSESSFHSS 352
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RESULT 11

US-09-647-501-2
; Sequence 2, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
; APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT APPLICATION NUMBER: US/09/647,501
; CURRENT FILING DATE: 2000-09-24
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-647-501-2

Query Match 89.9%; Score 1678.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.1e-132;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Db     64 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSGQDIS 185
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; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074033_us-10-785-230-3.rapbm.

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This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074033_us-10-785-230-3.rapbm.

[start](#)

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GenCore version 6.2
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OM protein - protein search, using sw model

Run on: February 6, 2007, 14:24:16 ; Search time 137 Seconds
(without alignments)
1215.298 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSIDNYSEEVGS.....KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1867	100.0	359	4 US-10-785-230-3	Sequence 3, Appli
2	1822	97.6	355	5 US-10-330-773-918	Sequence 918, App
3	1744.5	93.4	349	6 US-11-028-922A-2	Sequence 2, Appli
4	1678.5	89.9	352	3 US-09-953-692-2	Sequence 2, Appli
5	1678.5	89.9	352	3 US-09-953-717-2	Sequence 2, Appli
6	1678.5	89.9	352	3 US-09-104-063-4	Sequence 4, Appli
7	1678.5	89.9	352	3 US-09-813-651B-85	Sequence 85, Appl
8	1678.5	89.9	352	4 US-10-151-274-4	Sequence 4, Appli
9	1678.5	89.9	352	4 US-10-225-567A-76	Sequence 76, Appl
10	1678.5	89.9	352	4 US-10-245-850-1	Sequence 1, Appli

11	1678.5	89.9	352	4	US-10-251-703-38	Sequence 38, Appl
12	1678.5	89.9	352	4	US-10-021-660-123	Sequence 123, App
13	1678.5	89.9	352	4	US-10-014-322A-126	Sequence 126, App
14	1678.5	89.9	352	4	US-10-239-423-79	Sequence 79, Appl
15	1678.5	89.9	352	4	US-10-170-385-331	Sequence 331, App
16	1678.5	89.9	352	4	US-10-160-401-3	Sequence 3, Appli
17	1678.5	89.9	352	4	US-10-341-434-178	Sequence 178, App
18	1678.5	89.9	352	4	US-10-372-683-2	Sequence 2, Appli
19	1678.5	89.9	352	4	US-10-440-464-78	Sequence 78, Appl
20	1678.5	89.9	352	4	US-10-452-015-1	Sequence 1, Appli
21	1678.5	89.9	352	4	US-10-211-462-81	Sequence 81, Appl
22	1678.5	89.9	352	4	US-10-666-689-4	Sequence 4, Appli
23	1678.5	89.9	352	4	US-10-181-906-10	Sequence 10, Appl
24	1678.5	89.9	352	4	US-10-706-265-10	Sequence 10, Appl
25	1678.5	89.9	352	4	US-10-785-230-1	Sequence 1, Appli
26	1678.5	89.9	352	5	US-10-486-471-20	Sequence 20, Appl
27	1678.5	89.9	352	5	US-10-985-324-2	Sequence 2, Appli
28	1678.5	89.9	352	6	US-11-021-951-189	Sequence 189, App
29	1678.5	89.9	352	6	US-11-028-922A-1	Sequence 1, Appli
30	1672.5	89.6	352	3	US-09-826-509-485	Sequence 485, App
31	1672.5	89.6	352	5	US-10-925-095-485	Sequence 485, App
32	1672.5	89.6	356	5	US-10-723-860-1280	Sequence 1280, Ap
33	1670.5	89.5	352	3	US-09-870-759-37	Sequence 37, Appl
34	1670.5	89.5	352	3	US-09-870-759-144	Sequence 144, App
35	1670.5	89.5	352	3	US-09-751-708A-37	Sequence 37, Appl
36	1670.5	89.5	352	3	US-09-751-708A-144	Sequence 144, App
37	1670.5	89.5	352	4	US-10-428-817A-33	Sequence 33, Appl
38	1670.5	89.5	352	4	US-10-428-817A-140	Sequence 140, App
39	1670.5	89.5	352	5	US-10-937-758A-37	Sequence 37, Appl
40	1670.5	89.5	352	5	US-10-937-758A-121	Sequence 121, App
41	1641.5	87.9	352	5	US-10-791-592-6	Sequence 6, Appli
42	1641.5	87.9	352	5	US-10-791-166-6	Sequence 6, Appli
43	1633.5	87.5	348	5	US-10-330-773-921	Sequence 921, App
44	969.5	51.9	209	4	US-10-292-798-688	Sequence 688, App
45	964.5	51.7	209	4	US-10-017-161-790	Sequence 790, App

ALIGNMENTS

RESULT 1

US-10-785-230-3

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; Sequence 3, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadimitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10/785,230
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus
US-10-785-230-3
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Best Local Similarity 100.0%; Pred. No. 1.5e-160;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
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Db     61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
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          |||
Db      181 QGDISQGGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240

Qy      241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
          |||
Db      241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy      301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359
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Db      301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359

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RESULT 2

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US-10-330-773-918
; Sequence 918, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773.
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-330-773-918

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Query Match      97.6%; Score 1822; DB 5; Length 355;
Best Local Similarity 98.6%; Pred. No. 1.8e-156;
Matches 354; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

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Db      61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy      121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 180
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Db      121 N--KSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVS 178

Qy      181 QGDISQGGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240
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Db      179 QGDISQGGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQ 238

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Db      239 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITE--AFF 296

Qy      301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 359
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Db      297 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSVSTESESSSFHSS 355

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RESULT 3

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US-11-028-922A-2
; Sequence 2, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-028-922A-2

Query Match 93.4%; Score 1744.5; DB 6; Length 349;
Best Local Similarity 95.5%; Pred. No. 1.8e-149;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

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Db      1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRLKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
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Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db    236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGEFESVVKWISITEALAFFHCCLN 295

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    296 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 349
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RESULT 4

US-09-953-692-2

; Sequence 2, Application US/09953692
; Patent No. US20020107195A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1
; FILE REFERENCE: P50676C1
; CURRENT APPLICATION NUMBER: US/09/953,692
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-953-692-2

Query Match 89.9%; Score 1678.5; DB 3; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRLKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRLKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
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Db      179 EADDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy      246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db      239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy      306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
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Db      299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

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RESULT 5

US-09-953-717-2

; Sequence 2, Application US/09953717

; Patent No. US20020107196A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1{

; FILE REFERENCE: P50676D1

; CURRENT APPLICATION NUMBER: US/09/953,717

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 09/358,624

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Human

US-09-953-717-2

Query Match 89.9%; Score 1678.5; DB 3; Length 352;

Best Local Similarity 90.1%; Pred. No. 1.7e-143;

Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy      66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFKAVHVIYTVNLYSS 123

Qy      126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy      186 QGDDRYICDRLYPDSLWMVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
      : ||||| ||: ||:|||||||
Db      179 EADDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy      246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db      239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy      306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
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RESULT 6

US-09-104-063-4

; Sequence 4, Application US/09104063

; Patent No. US20020168356A1

; GENERAL INFORMATION:

; APPLICANT: Lee, James

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,063
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-104-063-4

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Query Match      89.9%; Score 1678.5; DB 3; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||:|:||||| ||||:| :|:||||| |||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||:|||||:|:||||| |||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADV SQGDIS 185
        |||||:|||||:|||||:|||||:| |||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGHGQKRKAL 245
        : ||||| ||: ||:|||||:|||||:|||||:|||||:|||||
Db    179 EADDRYICDRFYPNDLWVVVFQFHIMVGLILPGIVILSCYCIIISKLSHSGHGQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCGDFESIVHKWISITEALAFFHCCLN 305
        |||||:|||||:|||||:|||||:| |||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSSVTESESSSFHSS 359
        |||||:|||||:|:|||||:|||||:|||||
Db    299 PILYAFLGAKFKTSQAHALTSVSRGSSSLKILSKGKRGGHSSSVTESESSSFHSS 352

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RESULT 7
US-09-813-651B-85
; Sequence 85, Application US/09813651B
; Publication No. US20030018438A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol

```

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; APPLICANT: Tan Hehir, Christina
; APPLICANT: Kates, Steven
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-007
; CURRENT APPLICATION NUMBER: US/09/813,651B
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-651B-85
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Query Match      89.9%; Score 1678.5; DB 3; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;
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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
:|||||||:||||||| |||||||: ||:||||||| |||||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
|||||||:||||||| |||||||:||||||| |||||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVVWIPALLLTIPDFIFADV SQGDIS 185
|||||||:||||||| |||||||:||||||| |||||||:|||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYGVVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
: ||||||| ||: ||:||||||| |||||||:||||||| |||||||:|||||||
Db    179 EADDRYICDRFYNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
|||||||:||||||| |||||||:||||||| |||||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGKRGHSSSVTESESSSFHSS 359
|||||||:||||||| |||||||:||||||| |||||||:|||||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGHSSSVTESESSSFHSS 352
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RESULT 8

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US-10-151-274-4
; Sequence 4, Application US/10151274
; Publication No. US20030064071A1
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-274-4
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Query Match      89.9%; Score 1678.5; DB 4; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
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Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||:|:||||| ||||:| :|:||||| | |||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||:|||||:|:| | |||||:|||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
        |||||:|||||:|||||:|:| | |||||:|
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 245
        : ||||| | : ||: ||||| ||||| ||||| ||||| |||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        |||||:|||||:|||||:|:| | |||||:|:| | |||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
        |||||:||||| |:||||| ||||| ||||| |||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 9

US-10-225-567A-76

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; Sequence 76, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-76

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Query Match 89.9%; Score 1678.5; DB 4; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.7e-143;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||:|:||||| ||||:| :|:||||| | |||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||:|||||:|:| | |||||:|||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADVSQGDIS 185
        |||||:|||||:|||||:|:| | |||||:|
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 245
        : ||||| | : ||: ||||| ||||| ||||| ||||| |||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHKQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        |||||:|||||:|||||:|:| | |||||:|:| | |||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
        |||||:||||| |:||||| ||||| ||||| |||||

```

RESULT 10

US-10-245-850-1

; Sequence 1, Application US/10245850
; Publication No. US20030124628A1
; GENERAL INFORMATION:
; APPLICANT: Burns, Jennifer M.
; APPLICANT: Miao, Zhenhua
; APPLICANT: Wei, Zheng
; APPLICANT: Howard, Maureen C.
; APPLICANT: Premack, Brett A.
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting and Treating
; TITLE OF INVENTION: Diseases and Conditions Related to Chemokine Receptors
; FILE REFERENCE: 019934-003310US
; CURRENT APPLICATION NUMBER: US/10/245,850
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/338,100
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CXCR4 chemokine receptor
US-10-245-850-1

Query Match 89.9%; Score 1678.5; DB 4; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

Qy 6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
:|||||||:|:||||||| |||||:|: |:|:||||||| |||||:|||||||
Db 4 ISIIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy 66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy 126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy 186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
: ||||| ||: ||: |||||:|||||||:|||||||:|||||||:|||||||
Db 179 EADDRYICDRFYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 238

Qy 246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db 239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLN 298

Qy 306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
|||||||:||||||| |:|||||||:|||||||:|||||||:|||||||
Db 299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

RESULT 11

US-10-251-703-38

; Sequence 38, Application US/10251703
; Publication No. US20030148449A1
; GENERAL INFORMATION:
; APPLICANT: Kuliopulos, Athan
; APPLICANT: Covic, Lidiya
; TITLE OF INVENTION: G Protein Coupled Receptor Agonists and Antagonists and
; TITLE OF INVENTION: Methods of Activating and Inhibiting G Protein Coupled
; TITLE OF INVENTION: Receptors Using the Same
; FILE REFERENCE: NEMC-215 CIP
; CURRENT APPLICATION NUMBER: US/10/251,703
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 09/841,091
; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: 60/198,993
 ; PRIOR FILING DATE: 2000-04-21
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Pepducin
 ; OTHER INFORMATION: Peptide Sequence
 US-10-251-703-38

Query Match 89.9%; Score 1678.5; DB 4; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.7e-143;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||||:|:||||||| |||||:| :||:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPEFVAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPEFVAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVVWIPALLLTIPDFIFADV SQDIS 185
        |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
        : ||||| ||: ||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    179 EADDRYICDRFYPNDLWVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGCDFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 359
        |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFILGAKFKTSQAHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 12

US-10-021-660-123

; Sequence 123, Application US/10021660
 ; Publication No. US20030152926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynne, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: EOS Biotechnology, Inc.
 ; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
 ; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
 ; TITLE OF INVENTION: Modulators
 ; FILE REFERENCE: 018501-000710US
 ; CURRENT APPLICATION NUMBER: US/10/021,660
 ; CURRENT FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: US/09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/637,977
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 123
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-021-660-123

Query Match 89.9%; Score 1678.5; DB 4; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.7e-143;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||||:|:||||||| |||||:| :||:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
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Qy      66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNLYSS 123

Qy     126 VLILAFISLDryLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVsqGDIS 185
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     124 VLILAFISLDryLAIVHATNSQRPRKLLAEKVYVGWIPALLLTIPDFIFANV-----S 178

Qy     186 QGDDRYICDRlyPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKAL 245
         : ||||||| ||: ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     179 EADDRYICDRfYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKAL 238

Qy     246 KTTVILILAFfACWLPYYVGISIDSfILLGVIKQGCDfESIVHKWISITEALAFfHCCLN 305
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     239 KTTVILILAFfACWLPYYIGISIDSfILLEIIKQGCEfENTVHKWISITEALAFfHCCLN 298

Qy     306 PILYAFLGAKfKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 359
         |||||||:||||| |:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     299 PILYAFLGAKfKTSQAHALTSVRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 13

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US-10-014-322A-126
; Sequence 126, Application US/10014322A
; Publication No. US20030167129A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, Jr., John
; APPLICANT: Wilson, Carol
; APPLICANT: Tan Hehir, Christina
; APPLICANT: Kates, Steven
; APPLICANT: Krstenansky, John
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-008
; CURRENT APPLICATION NUMBER: US/10/014,322A
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/243,587
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/813,651
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/813,448
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-322A-126

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Query Match      89.9%; Score 1678.5; DB 4; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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```

Qy      6 VSIYTSdNYSEEVGSgDYDSNKEPCFRdENVHfNRIFLPTIYfIIFLTGIvGNGLVILVM 65
         :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4 ISIYTSdNYTEEMGSgDYDSMKEPCFREEnANfNKIFLPTIYSIIFLTGIvGNGLVILVM 63

Qy     66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAVANWYFGNfLCKAVHVIYTVNLYSS 123

Qy     126 VLILAFISLDryLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVsqGDIS 185
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     124 VLILAFISLDryLAIVHATNSQRPRKLLAEKVYVGWIPALLLTIPDFIFANV-----S 178

Qy     186 QGDDRYICDRlyPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKAL 245
         : ||||||| ||: ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     179 EADDRYICDRfYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLShSKGHQKRKAL 238

Qy     246 KTTVILILAFfACWLPYYVGISIDSfILLGVIKQGCDfESIVHKWISITEALAFfHCCLN 305
         |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     239 KTTVILILAFfACWLPYYIGISIDSfILLEIIKQGCEfENTVHKWISITEALAFfHCCLN 298

```


Qy 306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
 |||||:||||| |:|||||
 Db 299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

RESULT 14

US-10-239-423-79

; Sequence 79, Application US/10239423
 ; Publication No. US20030186889A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
 ; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
 ; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
 ; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
 ; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
 ; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
 ; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
 ; FILE REFERENCE: 022217us
 ; CURRENT APPLICATION NUMBER: US/10/239,423
 ; CURRENT FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: DE10016013.1
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn Ver.. 2.1
 ; SEQ ID NO 79
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
 US-10-239-423-79

Query Match 89.9%; Score 1678.5; DB 4; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.7e-143;
 Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

Qy 6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
 :|||||:||||| |||||:| :|:||||| |||||
 Db 4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
 Qy 66 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
 |||||:||||| :|:||||| |||||:|||||
 Db 64 GYQKRLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
 Qy 126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
 |||||:||||| |||||:||||| :|:||||| |||||:|||||
 Db 124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178
 Qy 186 QGDDRYICDRYPDSLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
 : ||||| ||: ||:||||| |||||:||||| |||||
 Db 179 EADDRYICDRYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238
 Qy 246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
 |||||:||||| :|||||:|: |||||:|||||
 Db 239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298
 Qy 306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
 |||||:||||| |:|||||
 Db 299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352

RESULT 15

US-10-170-385-331

; Sequence 331, Application US/10170385
 ; Publication No. US20030203372A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ward, Neil Raymond
 ; APPLICANT: Mundy, Christopher Robert
 ; APPLICANT: Kan, On
 ; APPLICANT: Harris, Robert Alan
 ; APPLICANT: White, Jonathan
 ; APPLICANT: Binley, Katie Mary
 ; APPLICANT: Rayner, William Nigel
 ; APPLICANT: Naylor, Stuart
 ; APPLICANT: Kingsman, Susan Mary

```
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-331
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Query Match      89.9%; Score 1678.5; DB 4; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.7e-143;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;
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```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
:|||||||:|:||||| ||||:| |:|:||||| ||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
|||||||:|:||||| ||||:| |:|:||||| ||||||
Db     64 GYQKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
|||||||:|:||||| ||||:| |:|:||||| ||||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
: ||||| | |: |:||||| ||||:| |:|:||||| ||||||
Db    179 EADDRYICDRFYNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFFHCCLN 305
|||||||:|:||||| ||||:| |:|:||||| ||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGHSSVSTESESSSFHSS 359
|||||||:|:||||| ||||:| |:|:||||| ||||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESESSSFHSS 352
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Search completed: February 6, 2007, 14:29:55
Job time : 137.834 secs
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start

SCORE 1.3 BuildDate: 11/17/2006

9	1678.5	89.9	352	6	US-10-511-937-3010	Sequence 3010, Ap
10	1678.5	89.9	352	6	US-10-219-051B-9078	Sequence 9078, Ap
11	1678.5	89.9	352	6	US-10-219-051B-9082	Sequence 9082, Ap
12	1678.5	89.9	352	7	US-11-371-354-68409	Sequence 68409, A
13	1678.5	89.9	363	6	US-10-545-557-19	Sequence 19, Appl
14	1672.5	89.6	352	7	US-11-404-939-485	Sequence 485, App
15	1633.5	87.5	348	6	US-10-540-898-921	Sequence 921, App
16	1210	64.8	230	7	US-11-437-734-4	Sequence 4, Appli
17	974	52.2	188	7	US-11-437-734-6	Sequence 6, Appli
18	969.5	51.9	209	7	US-11-214-063A-688	Sequence 688, App
19	584	31.3	368	6	US-10-511-937-2505	Sequence 2505, Ap
20	584	31.3	368	6	US-10-511-937-2931	Sequence 2931, Ap
21	584	31.3	368	7	US-11-302-678-59	Sequence 59, Appl
22	584	31.3	368	7	US-11-371-354-63307	Sequence 63307, A
23	570.5	30.6	360	6	US-10-581-413-1	Sequence 1, Appli
24	562.5	30.1	361	6	US-10-669-920-374	Sequence 374, App
25	562	30.1	359	6	US-10-219-051B-13793	Sequence 13793, A
26	551	29.5	364	6	US-10-669-920-377	Sequence 377, App
27	544.5	29.2	360	6	US-10-533-519-1184	Sequence 1184, Ap
28	544.5	29.2	360	6	US-10-219-051B-13795	Sequence 13795, A
29	544.5	29.2	360	7	US-11-242-111-19	Sequence 19, Appl
30	544.5	29.2	360	7	US-11-371-354-67277	Sequence 67277, A
31	537.5	28.8	374	6	US-10-669-920-3	Sequence 3, Appli
32	537.5	28.8	378	6	US-10-511-937-2404	Sequence 2404, Ap
33	537.5	28.8	389	6	US-10-545-557-23	Sequence 23, Appl
34	537.5	28.8	475	7	US-11-520-715-56811	Sequence 56811, A
35	534	28.6	357	7	US-11-371-354-66939	Sequence 66939, A
36	534	28.6	369	7	US-11-371-354-69405	Sequence 69405, A
37	533	28.5	355	6	US-10-516-032-8	Sequence 8, Appli
38	533	28.5	355	6	US-10-533-519-1109	Sequence 1109, Ap
39	533	28.5	355	7	US-11-371-354-56785	Sequence 56785, A
40	532	28.5	367	7	US-11-392-789-2	Sequence 2, Appli
41	528	28.3	369	7	US-11-404-939-481	Sequence 481, App
42	525.5	28.1	350	7	US-11-371-354-61621	Sequence 61621, A
43	522.5	28.0	350	7	US-11-371-354-68399	Sequence 68399, A
44	519.5	27.8	374	6	US-10-669-920-6	Sequence 6, Appli
45	512.5	27.5	325	6	US-10-669-920-237	Sequence 237, App

ALIGNMENTS

RESULT 1

US-11-437-734-2

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; Sequence 2, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: IIZASA, Hisashi
; APPLICANT: YOSHIDA, Nobuaki
; APPLICANT: NAKAJIMA, Toshihiro
; APPLICANT: YOSHIE, Osamu
; TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
; FILE REFERENCE: 1422-386P
; CURRENT APPLICATION NUMBER: US/11/437,734
; CURRENT FILING DATE: 2006-05-22
; PRIOR APPLICATION NUMBER: US/09/367,052
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-437-734-2
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Query Match      100.0%; Score 1867; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEPISVSIYTSNDYSEEVGSGDYSDNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
          |||
Db      1 MEPISVSIYTSNDYSEEVGSGDYSDNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
```

```

Qy      61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIYTV 120
        |||
Db      61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy     121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 180
        |||
Db     121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 180

Qy     181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSHKGHQ 240
        |||
Db     181 QGDISQGDDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSHKGHQ 240

Qy     241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFFESIVHKWISITEALAFF 300
        |||
Db     241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFFESIVHKWISITEALAFF 300

Qy     301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESSESSFHSS 359
        |||
Db     301 HCCLNPILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESSESSFHSS 359

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RESULT 2

US-11-437-734-8

```

; Sequence 8, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: IIZASA, Hisashi
; APPLICANT: YOSHIDA, Nobuaki
; APPLICANT: NAKAJIMA, Toshihiro
; APPLICANT: YOSHIE, Osamu
; TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
; FILE REFERENCE: 1422-386P
; CURRENT APPLICATION NUMBER: US/11/437,734
; CURRENT FILING DATE: 2006-05-22
; PRIOR APPLICATION NUMBER: US/09/367,052
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-437-734-8

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Query Match      98.2%; Score 1834; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-165;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      8 IYTSNDYSEEVSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 67
        |||
Db      1 IYTSNDYSEEVSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 60

Qy     68 QKKLRSMTDKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 127
        |||
Db     61 QKKLRSMTDKYRLHLSVADLLFVITLPPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 120

Qy     128 ILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSQGDISQG 187
        |||
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVSQGDISQG 180

Qy     188 DDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSHKGHQKRKALKT 247
        |||
Db     181 DDRYICDRLYPDSLWMVVFQFHIMVGLILPGIVILSCYCIISKLSHSHKGHQKRKALKT 240

Qy     248 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFFESIVHKWISITEALAFFHCCCLNPI 307
        |||
Db     241 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFFESIVHKWISITEALAFFHCCCLNPI 300

Qy     308 LYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESSESSFHSS 359
        |||
Db     301 LYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESSESSFHSS 352

```

RESULT 3

US-10-540-898-918
; Sequence 918, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-540-898-918

Query Match 97.6%; Score 1822; DB 6; Length 355;
Best Local Similarity 98.6%; Pred. No. 2e-164;
Matches 354; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

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QY      1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60
          |||
Db      1 MEPISVSIYTS DNYSEEVGSGDYDSNKEPCFRDENVHFNRI FLPTIYFIIFLTGIVGNGL 60

QY      61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
          |||
Db      61 VILVMGYQKKLRSM TDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

QY      121 NLYSSVLILAFISLD RYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 180
          | |||
Db      121 N--KSVLILAFISLD RYLAIVHATNSQRPRKLLAEKAVYVGWIPALLLTIPDFIFADVS 178

QY      181 QGDISQGDDRYICDR LYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQ 240
          |||
Db      179 QGDISQGDDRYICDR LYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSKGHQ 238

QY      241 KRKALKTTVILILAF FACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITEALAFF 300
          |||
Db      239 KRKALKTTVILILAF FACWLPYYVGISIDSFILLGVIKQGCD FESIVHKWISITE--AFF 296

QY      301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGS SLKILSKGKRGGHSSVSTESESSSFHSS 359
          |||
Db      297 HCCLNPILYAFLGAKFKSSAQHALNSMSRGS SLKILSKGKRGGHSSVSTESESSSFHSS 355
```

RESULT 4

US-10-219-051B-9076
; Sequence 9076, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9076
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / 008565
; DATABASE ENTRY DATE: 2001-10-16

US-10-219-051B-9076

Query Match 93.4%; Score 1744.5; DB 6; Length 349;
Best Local Similarity 95.5%; Pred. No. 4.2e-157;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

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Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      : |||
Db      1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||
Db     61 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADV SQGDIS 185
      |||
Db    121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYGVWIPALLLTIPDIIFADV-----S 175

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
      |||
Db    176 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 235

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
      |||
Db    236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVKWISITEALAFFHCCLN 295

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSSVTESESSSFHSS 359
      |||
Db    296 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSSVTESESSSFHSS 349
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RESULT 5

US-10-219-051B-9080

; Sequence 9080, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9080
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
; DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9080

Query Match 93.4%; Score 1744.5; DB 6; Length 349;
Best Local Similarity 95.5%; Pred. No. 4.2e-157;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      : |||
Db      1 MEIYTSNDYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy     66 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||
Db     61 GYQKLRSMtdKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADV SQGDIS 185
      |||
Db    121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYGVWIPALLLTIPDIIFADV-----S 175

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
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Db      176 QGDGRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 235
Qy      246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
Db      236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGEFESVVKWISITEALAFFHCCLN 295
Qy      306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
Db      296 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349

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RESULT 6

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US-10-505-928-745
; Sequence 745, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 745
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-745

```

```

Query Match      89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```

```

Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
Db      4 ISIIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
Qy     66 GYQKRLRSMTDKYRLHLSVADLLFVITLFPWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
Db     64 GYQKRLRSMTDKYRLHLSVADLLFVITLFPWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADV SQGDIS 185
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178
Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 245
Db    179 EADDRIYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 238
Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITEALAFFHCCLN 298
Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

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RESULT 7

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US-10-511-937-2486
; Sequence 2486, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

```



```
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2486
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2486
```

```
Query Match          89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;
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```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMtdKYRLHLSVADLLFVITLpFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKKLRSMtdKYRLHLSVADLLFVITLpFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDryLAIVHATNSQRPRKLLAEKAVYGVGWIPALLLTIPDFIFADVSGQDIS 185
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    124 VLILAFISLDryLAIVHATNSQRPRKLLAEKVYGVGWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
       : ||||| ||: ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    179 EADDRYICDRYPNDLWVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSfILLGVikQGCDfESIVHKWISITEALAFFHCCLN 305
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    239 KTTVILILAFFACWLPYYIGISIDSfILLEIKQGCEfENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 359
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

```
RESULT 8
US-10-511-937-2935
; Sequence 2935, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-511-937-2935

Query Match 89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||||:|:||||||| |||||:| :|:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||||:|||||||:|:||||| |||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
        |||||:|||||||:|||||||:|||||||:| |||||
Db    124 VLILAFISLDRYLAIIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 245
        : ||||| ||: ||:||||||| |||||:||||||| |||||:|||||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHQRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
        |||||:|||||||:|||||||:|||||||:| |||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSSVTESESSSFHSS 359
        |||||:|||||||:|||||||:|||||||:|||||||
Db    299 PILYAFILGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSSVTESESSSFHSS 352
```

RESULT 9

US-10-511-937-3010

; Sequence 3010, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3010
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-3010

Query Match 89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
        :|||||||:|:||||||| |||||:| :|:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
        |||||:|||||||:|||||||:|:||||| |||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
```



```
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9082
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9082
```

```
Query Match      89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;
```

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      :|||||:|:||||| |||||:| :|:||||| |||||:|||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFKLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYGVWIPALLLTIPDFIFADV SQGDIS 185
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYGVWIPALLLTIPDFIFANV-----S 178

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 245
      : ||||| ||: ||:|||||:|||||:|||||:|||||:|||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIISKLSHSGHGQKRKAL 238

Qy    246 KTTVILILAFFACWLPPYYVIGISIDSFILLGVIKQGCD FESIVHKWISITEALAFFHCCLN 305
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    239 KTTVILILAFFACWLPPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFLGAKFKSSAQHALNSMRGSSSLKIILSKGKRGGHSSSVSTESSESSSFHSS 359
      |||||:||||| |:|||||:|||||:|||||:|||||
Db    299 PILYAFLGAKFKTSAQHALTSVSRGSSSLKIILSKGKRGGHSSSVSTESSESSSFHSS 352
```

```
RESULT 12
US-11-371-354-68409
; Sequence 68409, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
```

; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68409
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-68409

Query Match 89.9%; Score 1678.5; DB 7; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
         :|||||||:|:||||||| |||||:|: ||:||||||| |||||:|||||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
         |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db     64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy    126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSGQDIS 185
         |||||:||||||| |||||:||||||| |||||:||||||| |||||:|
Db    124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV----S 178

Qy    186 QGDDRYICDRLYPDSLWMVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 245
         : ||||| ||: ||:||||||| |||||:||||||| |||||:|||||||
Db    179 EADDRYICDRFYPNDLWVVVFQFQHMVGLILPGIVILSCYCIISKLSHSGHQKRKAL 238

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDVESIVHKWISITEALAFFHCCLN 305
         |||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db    239 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGRGGHSSSVTESESSSFHSS 359
         |||||:||||||| ||:||||||| |||||:||||||| |||||:|||||||
Db    299 PILYAFILGAKFKTSAQHALTSVSRGSSLKILSKGRGGHSSSVTESESSSFHSS 352
```

RESULT 13

US-10-545-557-19

; Sequence 19, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:
; APPLICANT: ANOSYS
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING ANTIBODY
; TITLE OF INVENTION: REPERTOIRES
; FILE REFERENCE: 3665-158
; CURRENT APPLICATION NUMBER: US/10/545,557
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: PCT/IB2004/000888
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US60/447,291
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 363
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CXCR4 + HA Tag
US-10-545-557-19

Query Match 89.9%; Score 1678.5; DB 6; Length 363;
Best Local Similarity 90.1%; Pred. No. 7.9e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
         :|||||||:|:||||||| |||||:|: ||:||||||| |||||:|||||||
Db     15 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 74

Qy     66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
         |||||:|||||||:|||||||:|||||||:|||||||:|||||||
```


US-10-540-898-921
 ; Sequence 921, Application US/10540898
 ; Publication No. US20060166213A1
 ; GENERAL INFORMATION:
 ; APPLICANT: David W. Morris
 ; APPLICANT: Marc Malandro
 ; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
 ; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
 ; CURRENT APPLICATION NUMBER: US/10/540,898
 ; CURRENT FILING DATE: 2005-06-27
 ; PRIOR APPLICATION NUMBER: US 10/330,773
 ; PRIOR FILING DATE: 2002-12-27
 ; NUMBER OF SEQ ID NOS: 981
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 921
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-540-898-921

Query Match 87.5%; Score 1633.5; DB 6; Length 348;
 Best Local Similarity 88.7%; Pred. No. 1.4e-146;
 Matches 314; Conservative 19; Mismatches 12; Indels 9; Gaps 3;

```

Qy      6 VSIYTSNDYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
      :|||||||:|:||||| |||||:| :|:||||| |||||:|||||
Db      4 ISIYTSNDYTEEMGSGDYDSMKEPCFREANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy     66 GYQKRLSMTDKYRLHLSVADLLFVITLPEWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
      |||||:|||||:|||||:|||||:|||||:|||||
Db     64 GYQKRLSMTDKYRLHLSVADLLFVITLPEWAVDAVANWYFGNFKAVHVIYTVN--KS 121

Qy    126 VLILAFISLDRLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
      |||||:|||||:|||||:|||||:|||||:|||||
Db    122 VLILAFISLDRLAIVHATNSQRPRKLLAEKVYVGVWIPALLLTIPDFIFANV-----S 176

Qy    186 QGDDRYICDRYPDSLWMVVFQFQHMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 245
      : ||||| ||: ||:|||||:|||||:|||||:|||||:|||||
Db    177 EADDRYICDRFYPNDLWVVVFQFQHMVGLILPGIVILSCYCIISKLSHSKGHQKRKAL 236

Qy    246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
      |||||:|||||:|||||:|||||:|||||:|||||
Db    237 KTTVILILAFFACWLPYYIGISIDSFILLEIKQGEFENTVHKWISITE--AFFHCCLN 294

Qy    306 PILYAFILGAKFKSSAQHALNSMRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
      |||||:|||||:|||||:|||||:|||||:|||||
Db    295 PILYAFILGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 348
  
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Search completed: February 6, 2007, 14:31:23
 Job time : 42.4037 secs

start

SCORE 1.3 BuildDate: 11/17/2006
